

## Sequence Listing

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Gao, Wei-Qiang  
Gerber, Hanspeter  
Gerritsen, Mary E.  
Goddard, Audrey  
Godowski, Paul J.  
Grimaldi, J. Christopher  
Gurney, Austin L.  
Hillan, Kenneth J  
Kljavin, Ivar J.  
Kuo, Sophia S.  
Napier, Mary A.  
Pan, James;  
Paoni, Nicholas F.  
Roy, Margaret Ann  
Shelton, David L.  
Stewart, Timothy A.  
Tumas, Daniel  
Williams, P. Mickey  
Wood, William I.



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Cys Met Ala Leu Ser Leu Thr Leu Cys Phe Val Met Phe Trp Thr  
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Pro Asn Val Ser Glu Lys Ile Leu Ile Asp Ile Ile Gly Val Asp  
350 355 360

Phe Ala Phe Ala Glu Leu Cys Val Val Pro Leu Arg Ile Phe Ser  
365 370 375

Phe Phe Pro Val Pro Val Thr Val Arg Ala His Leu Thr Gly Trp  
380 385 390

Leu Met Thr Leu Lys Lys Thr Phe Val Leu Ala Pro Ser Ser Val  
395 400 405

Leu Arg Ile Ile Val Leu Ile Ala Ser Leu Val Val Leu Pro Tyr  
410 415 420

Leu Gly Val His Gly Ala Thr Leu Gly Val Gly Ser Leu Leu Ala  
425 430 435

Gly Phe Val Gly Glu Ser Thr Met Val Ala Ile Ala Ala Cys Tyr  
440 445 450

Val Tyr Arg Lys Gln Lys Lys Lys Met Glu Asn Glu Ser Ala Thr  
455 460 465

Glu Gly Glu Asp Ser Ala Met Thr Asp Met Pro Pro Thr Glu Glu  
470 475 480

Val Thr Asp Ile Val Glu Met Arg Glu Glu Asn Glu  
485 490

<210> 8

<211> 535

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 33, 66, 96, 387

<223> unknown base

<400> 8

cctgacagaa gtgccccgga gctgggggag atncaacatt aagaagatgc 50

tgagcttctg gtgcntttg gctctaattc tggccacaca gagaancagt 100

cggcctattg tcaacctctt tgttcccgg gaccttggtg gcagttctgc 150

agccacagag gcagtggcga tttgacagc cacataccct gtgggtcaca 200

tgccatacgg ctggttgacg gaaatccgtg ctgtgtatcc tgctttcgac 250

aagaataacc ccagcaacaa actggtgagc acgagcaaca cagtcacggc 300

ggcccacatc aagaagtica ccttcgtctg catggctctg tcactcacgc 350

tctgtttcgt gatgttttgg acaccaacg tgtctngaa aatcttgata 400

gacatcatcg gaggtagactt tgcctttgca gaactctgtg ttgttccttt 450

gcggatcttc tccttctcc cagttccagt cacagtgagg gcgcactca 500

ccgggtggct gatgacactg aagaaaacct tcgtc 535

<210> 9

<211> 434

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 32, 54, 80, 111, 117, 122, 139, 193, 205, 221, 226, 228, 273,  
293, 296, 305, 336, 358, 361

<223> unknown base

<400> 9

tgacggaatc ccgggctggg tatcctggtt tngacaagat aaacccccag 50

caanaaattg gggagcaggg caaaacagtn acgggcagcc cacatcaaga 100

agttcacctt ngtttgnatg gntctgtcaa ctcacgctnt gtttcgtgat 150

gttttgaca cccaaagtgt ttgagaaaat ttgatagac atnatcgag 200

tggantttgc ctttgagaa ntttngntg ttccttgcg gattttctcc 250

ttttcccg ttccagtcac agngaggcg catctaccg ggnggntgat 300

gacantgaag aaaaccttg tccttgcccc cagctntttg gtgcggatca 350

ttgtcctnat ngccagcctt gtggtcctac cctacctggg ggtgcacggt 400

gcgaccctgg gcgtgggttc cctctggcg ggca 434

<210> 10

<211> 154

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 33, 49, 68, 83, 90, 98, 119

<223> unknown base

<400> 10

tattcccagt tccggtcacg gggagggcgc atntcaccgg gtggctgang 50

aaactgaaga aaacctngt ccttgcccc agntttgtgn tgcggatnat 100

cgctctcatc gccagcctng tggctctacc ctacctgggg gtgcacggtg 150

agac 154

<210> 11

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 11

ctgatccggt tcttggtgcc cctg 24

<210> 12

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 12

gctctgtcac tcacgctc 18

<210> 13

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 13

tcattcttc cctctccc 18

<210> 14

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 14

ccttccgcca cggagttc 18

<210> 15

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 15

ggcaaagtcc actccgatga tgtc 24

<210> 16

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 16

gcctgctgtg gtcacaggtc tccg 24

<210> 17

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 17

tcgggggagca ggccttgaac cggggcattg ctgctgtcaa ggagg 45

<210> 18

<211> 1901

<212> DNA

<213> Homo sapiens

<400> 18

gccccgcgcc cggcgccggg cccccgaagc cgggagccac cgccatgggg 50

gcctgcctgg gagcctgtc cctgtcagc tgcgcgtcct gcctctgcgg 100

ctctgcccc tgcacctgt gcagctgtg ccccgccagc cgcaactcca 150

ccgtgagccg cctcatcttc acgttcttc tcttctggg ggtgctggtg 200

tccatcatta tgctgagccc gggcgtggag agtcagctct acaagctgcc 250

ctgggtgtgt gaggaggggg ccgggatccc caccgtctg cagggccaca 300

tcgactgtgg ctccctgctt ggctaccgcg ctgtctaccg catgtgcttc 350

gccacggcgg ccttctctt ctcttttc accctgtca tgctctgcgt 400

gagcagcagc cgggaccccc gggctgcat ccagaatggg ttttggtct 450

ttaagttct gatcctggtg ggcctaccg tgggtgcctt ctacatccct 500

gacggctct tcaccaacat ctggtctac ttcggcgtcg tgggtcctt 550

cctcttcac ctcatccagc tgggtgtgt catcgacttt gcgcactct 600

ggaaccagcg gtggtgggc aaggccgagg agtgcgattc ccgtgcctgg 650

tacgcagcc tcttctctt cactctctc ttctactgc tgcgatcgc 700

ggccgtggcg ctgatgtca tgtactacac tgagccagc ggctgccacg 750

agggcaaggt ctcatcagc ctcaacctca cttctgtgt ctgcgtgcc 800

atcgctgtg tctgccccaa ggtccaggac gccagccca actcgggtct 850

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cagaccgagg agtggccacc tatgctagac gccacacagc agcagcagca 1150

gcagggtggca gcctgtgagg gccgggcctt tgacaacgag caggacggcg 1200

tcacctacag ctactccttc ttccattct gcctggtgct ggcctcactg 1250

cacgtcatga tgacgtcac caactggtac aagcccgggtg agaccggaa 1300

gatgatcagc acgtggaccg ccgtgtgggt gaagatctgt gccagctggg 1350

cagggtgct cctctacctg tggaccctgg tagcccaact cctcctgcgc 1400

aaccgcgact tcagctgagg cagcctcaca gcctgccatc tggtcctcc 1450

tgccacctgg tgctctcgg ctcggtgaca gccaacctgc cccctccca 1500

caccaatcag ccaggctgag cccccaccc tgcaccagct ccaggacctg 1550

cccctgagcc gggccttcta gtcgtagtgc cttcagggtc cgaggagcat 1600

caggctctg cagagcccca tcccccgcc acaccacac ggtggagctg 1650

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ggggaactcc caccacagt gggcatccgg cactgaagcc ctggtgttc 1800

tgtcacgtc cccagggga ccctgcccc ttctggact tcgtgcctta 1850

ctgagtctct aagactttt ctaataaaca agccagtgcg tgtaaaaaa 1900

a 1901

<210> 19

<211> 457

<212> PRT

<213> Homo sapiens

<400> 19

Met Gly Ala Cys Leu Gly Ala Cys Ser Leu Leu Ser Cys Ala Ser

1

5

10

15

Cys Leu Cys Gly Ser Ala Pro Cys Ile Leu Cys Ser Cys Cys Pro

20

25

30

Ala Ser Arg Asn Ser Thr Val Ser Arg Leu Ile Phe Thr Phe Phe  
35 40 45

Leu Phe Leu Gly Val Leu Val Ser Ile Ile Met Leu Ser Pro Gly  
50 55 60

Val Glu Ser Gln Leu Tyr Lys Leu Pro Trp Val Cys Glu Glu Gly  
65 70 75

Ala Gly Ile Pro Thr Val Leu Gln Gly His Ile Asp Cys Gly Ser  
80 85 90

Leu Leu Gly Tyr Arg Ala Val Tyr Arg Met Cys Phe Ala Thr Ala  
95 100 105

Ala Phe Phe Phe Phe Phe Thr Leu Leu Met Leu Cys Val Ser  
110 115 120

Ser Ser Arg Asp Pro Arg Ala Ala Ile Gln Asn Gly Phe Trp Phe  
125 130 135

Phe Lys Phe Leu Ile Leu Val Gly Leu Thr Val Gly Ala Phe Tyr  
140 145 150

Ile Pro Asp Gly Ser Phe Thr Asn Ile Trp Phe Tyr Phe Gly Val  
155 160 165

Val Gly Ser Phe Leu Phe Ile Leu Ile Gln Leu Val Leu Leu Ile  
170 175 180

Asp Phe Ala His Ser Trp Asn Gln Arg Trp Leu Gly Lys Ala Glu  
185 190 195

Glu Cys Asp Ser Arg Ala Trp Tyr Ala Gly Leu Phe Phe Phe Thr  
200 205 210

Leu Leu Phe Tyr Leu Leu Ser Ile Ala Ala Val Ala Leu Met Phe  
215 220 225

Met Tyr Tyr Thr Glu Pro Ser Gly Cys His Glu Gly Lys Val Phe  
230 235 240

Ile Ser Leu Asn Leu Thr Phe Cys Val Cys Val Ser Ile Ala Ala  
245 250 255



Val Leu Pro Lys Val Gln Asp Ala Gln Pro Asn Ser Gly Leu Leu  
260 265 270

Gln Ala Ser Val Ile Thr Leu Tyr Thr Met Phe Val Thr Trp Ser  
275 280 285

Ala Leu Ser Ser Ile Pro Glu Gln Lys Cys Asn Pro His Leu Pro  
290 295 300

Thr Gln Leu Gly Asn Glu Thr Val Val Ala Gly Pro Glu Gly Tyr  
305 310 315

Glu Thr Gln Trp Trp Asp Ala Pro Ser Ile Val Gly Leu Ile Ile  
320 325 330

Phe Leu Leu Cys Thr Leu Phe Ile Ser Leu Arg Ser Ser Asp His  
335 340 345

Arg Gln Val Asn Ser Leu Met Gln Thr Glu Glu Cys Pro Pro Met  
350 355 360

Leu Asp Ala Thr Gln Gln Gln Gln Gln Val Ala Ala Cys Glu  
365 370 375

Gly Arg Ala Phe Asp Asn Glu Gln Asp Gly Val Thr Tyr Ser Tyr  
380 385 390

Ser Phe Phe His Phe Cys Leu Val Leu Ala Ser Leu His Val Met  
395 400 405

Met Thr Leu Thr Asn Trp Tyr Lys Pro Gly Glu Thr Arg Lys Met  
410 415 420

Ile Ser Thr Trp Thr Ala Val Trp Val Lys Ile Cys Ala Ser Trp  
425 430 435

Ala Gly Leu Leu Leu Tyr Leu Trp Thr Leu Val Ala Pro Leu Leu  
440 445 450

Leu Arg Asn Arg Asp Phe Ser  
455

<210> 20

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 20

gccgcctcat cttcacgttc ttcc 24

<210> 21

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 21

tcatccagct ggtgctgctc 20

<210> 22

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 22

cttcttcac ttctgcctgg 20

<210> 23

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 23

cctgggcaaa aatgcaac 18

<210> 24

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 24

caggaatgta gaaggcaccc acgg 24

<210> 25

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 25

tggcacagat cttcacccac acgg 24

<210> 26

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 26

tgtccatcat tatgtgagc ccgggcgtgg agagtcagct ctacaagctg 50

<210> 27

<211> 1351

<212> DNA

<213> Homo sapiens

<400> 27

gagcgaggcc ggggactgaa ggtgtgggtg tcgagccctc tggcagaggg 50

ttaacctggg tcaaatgcac ggattctcac ctcgtacagt tacgctctcc 100

cgcggcacgt ccgcgaggac ttgaagtcct gagcgctcaa gttgtccgt 150

aggtcgagag aaggccatgg aggtgccgcc accggcacccg cggagctttc 200

tctgtagagc attgtgccta tttccccgag tctttgctgc cgaagctgtg 250

actgccgatt cggaagtcct tgaggagcgt cagaagcggc ttcctacgt 300

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ttggcaaaga tgaacagcag agaattcaa aggaccttgc taatatctgt 400  
aagacggcag ctacagcagg catcattggc tgggtgtatg ggggaatacc 450  
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ttaatctatc aatatatgca tacatggata tatccacca cctagatttt 1300  
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<211> 285

<212> PRT

<213> Homo sapiens

<400> 28

Met Glu Val Pro Pro Pro Ala Pro Arg Ser Phe Leu Cys Arg Ala  
1 5 10 15

Leu Cys Leu Phe Pro Arg Val Phe Ala Ala Glu Ala Val Thr Ala  
20 25 30

Asp Ser Glu Val Leu Glu Glu Arg Gln Lys Arg Leu Pro Tyr Val  
35 40 45

Pro Glu Pro Tyr Tyr Pro Glu Ser Gly Trp Asp Arg Leu Arg Glu  
50 55 60

Leu Phe Gly Lys Asp Glu Gln Gln Arg Ile Ser Lys Asp Leu Ala  
65 70 75

Asn Ile Cys Lys Thr Ala Ala Thr Ala Gly Ile Ile Gly Trp Val  
80 85 90

Tyr Gly Gly Ile Pro Ala Phe Ile His Ala Lys Gln Gln Tyr Ile  
95 100 105

Glu Gln Ser Gln Ala Glu Ile Tyr His Asn Arg Phe Asp Ala Val  
110 115 120

Gln Ser Ala His Arg Ala Ala Thr Arg Gly Phe Ile Arg Tyr Gly  
125 130 135

Trp Arg Trp Gly Trp Arg Thr Ala Val Phe Val Thr Ile Phe Asn  
140 145 150

Thr Val Asn Thr Ser Leu Asn Val Tyr Arg Asn Lys Asp Ala Leu  
155 160 165

Ser His Phe Val Ile Ala Gly Ala Val Thr Gly Ser Leu Phe Arg  
170 175 180

Ile Asn Val Gly Leu Arg Gly Leu Val Ala Gly Gly Ile Ile Gly  
185 190 195

Ala Leu Leu Gly Thr Pro Val Gly Gly Leu Leu Met Ala Phe Gln

200	205	210
Lys Tyr Ala Gly Glu Thr Val Gln Glu Arg Lys Gln Lys Asp Arg		
215	220	225
Lys Ala Leu His Glu Leu Lys Leu Glu Glu Trp Lys Gly Arg Leu		
230	235	240
Gln Val Thr Glu His Leu Pro Glu Lys Ile Glu Ser Ser Leu Arg		
245	250	255
Glu Asp Glu Pro Glu Asn Asp Ala Lys Lys Ile Glu Ala Leu Leu		
260	265	270
Asn Leu Pro Arg Asn Pro Ser Val Ile Asp Lys Gln Asp Lys Asp		
275	280	285

<210> 29  
 <211> 324  
 <212> DNA  
 <213> Homo sapiens

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 ctattacccg gaatctggat gggaccgctc cgggagctgt ttggcaaaga 100  
 tgaacagcag agaatttcaa aggaccttgc taatatctgt aagacggcag 150  
 ctacagcagg catcattggc tgggtgtatg ggggaatacc agcttttatt 200  
 catgctaaac aacaatacat tgagcagagc caggcagaaa ttatcataa 250  
 ccggtttgat gctgtgcaat ctgcacatcg tgctgccaca cgaggcttca 300  
 ttcgttcatt gctggcgccg aacc 324

<210> 30  
 <211> 377  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 262, 330, 371

<223> unknown base

<400> 30

tcaagtttgt ccgtaggtcg agagaaggcc atggaggtgc cgccaccggc 50

accgcgagc tttttctgt agagcattgt gcctatttcc ccgagtttt 100

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gcggttccc tacgtcccag agccctatta cccggaattt ggatgggacc 200

gcctccggga gctgtttggc aaagatgaac agcagagaat ttcaaaggac 250

cttgctgata tntgtaagac ggcagctaca gcaggcatca ttgctgggt 300

gtatggggga ataccagctt ttattcatgn taaacaacaa tacattgagc 350

agagccaggc agaaatttat nataacc 377

<210> 31

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 31

tcgtacagtt acgtctccc 20

<210> 32

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 32

cttgaggagc gtcagaagcg 20

<210> 33

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 33

ataacgaatg aagcctcgtg 20

<210> 34

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 34

gctaatatct gtaagacggc agctacagca ggcatcattg 40

<210> 35

<211> 1819

<212> DNA

<213> Homo sapiens

<400> 35

gagccgcccgc cgcgcgcgcgc cgcgcactg cagccccagg ccccgcccc 50

ccaccacgt ctgcgttgc gccccgcctg ggccaggccc caaaggcaag 100

gacaaagcag ctgtcaggga acctccgccg gagtccaatt tacgtgcagc 150

tgccggcaac cacagggtcc aagatggttt gcgggggctt cgcgtgttcc 200

aagaactgcc tgtgcgccct caacctgctt tacaccttgg ttagtctgct 250

gctaattgga attgctgcgt ggggcattgg ctgcgggctg atttccagtc 300

tccgagtggc cggcgtgggc attgcagtgg gcattcttct gttcctgatt 350

gctttagtgg gtctgattgg agctgtaaaa catcatcagg tgttgctatt 400

ttttatatg attattctgt tacttgtatt tattgttcag ttttctgat 450

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gttggttgga acaatacggc aagtgctcga aatgacatcc agagaaatct 550



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ctagaaatag ttatgtctta ggaaattgtg gttaatttt tgacttttac 1400  
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aagtatatct atatgatctt gatattgttt tataataatt tgaagtctaa 1550  
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gttaaaaaat taaaggacag aaacctttct ttgtgtatgc atgtttgaat 1800

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<210> 36

<211> 204

<212> PRT

<213> Homo sapiens

<400> 36

Met Val Cys Gly Gly Phe Ala Cys Ser Lys Asn Cys Leu Cys Ala  
1 5 10 15

Leu Asn Leu Leu Tyr Thr Leu Val Ser Leu Leu Leu Ile Gly Ile  
20 25 30

Ala Ala Trp Gly Ile Gly Phe Gly Leu Ile Ser Ser Leu Arg Val  
35 40 45

Val Gly Val Val Ile Ala Val Gly Ile Phe Leu Phe Leu Ile Ala  
50 55 60

Leu Val Gly Leu Ile Gly Ala Val Lys His His Gln Val Leu Leu  
65 70 75

Phe Phe Tyr Met Ile Ile Leu Leu Leu Val Phe Ile Val Gln Phe  
80 85 90

Ser Val Ser Cys Ala Cys Leu Ala Leu Asn Gln Glu Gln Gln Gly  
95 100 105

Gln Leu Leu Glu Val Gly Trp Asn Asn Thr Ala Ser Ala Arg Asn  
110 115 120

Asp Ile Gln Arg Asn Leu Asn Cys Cys Gly Phe Arg Ser Val Asn  
125 130 135

Pro Asn Asp Thr Cys Leu Ala Ser Cys Val Lys Ser Asp His Ser  
140 145 150

Cys Ser Pro Cys Ala Pro Ile Ile Gly Glu Tyr Ala Gly Glu Val  
155 160 165

Leu Arg Phe Val Gly Gly Ile Gly Leu Phe Phe Ser Phe Thr Glu  
170 175 180

Ile Leu Gly Val Trp Leu Thr Tyr Arg Tyr Arg Asn Gln Lys Asp  
185 190 195

Pro Arg Ala Asn Pro Ser Ala Phe Leu  
200

<210> 37  
<211> 390  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 20, 35, 61, 83, 106, 130, 133, 187, 232, 260, 336  
<223> unknown base

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tagccntgaa ccaggagcaa cagggtcagn ttntggaggt tgggtggaac 150  
  
aatacggcaa gtgctcgaaa tgacatccag agaaatntaa actgctgtgg 200  
  
gttccgaagt gttaacccaa atgacacctg tntggctagc tgtgttaaaa 250  
  
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<210> 38  
<211> 566  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 27  
<223> unknown base

<400> 38

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ttttgactt ttacaggtaa gtgcaaagga gaagtgggtt catgaaatgt 200

tctaattgat aataacattt accttcagcc tccatcaga atggaacgag 250

ttttgagtaa tccaggaagt atatctatat gatcttgata ttgtttata 300

taattgaag tctaaaagac tgcattttta aacaagttag tattaatgcg 350

ttggcccacg tagcaaaaag atatttgatt atcttaaaaa ttgttaaata 400

ccgttttcat gaaagttctc agtattgtaa cagcaacttg tcaaacctaa 450

gcataattga atatgatctc ccataatttg aaattgaaat cgtatttgt 500

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gttgtgcccc acttgc 566

<210> 39

<211> 264

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 84-85, 206

<223> unknown base

<400> 39

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tggttggtcaa caatcacggc caagtgactc cgcaaatgac atcccagaga 150

aatcctaaac tgctgtgggt tccgaagtgt taacccaaat gacacctgtc 200

tggctngctg tgttaaaagt gaccactcgt gctcgccatg tgctccaatc 250

ataggagaat atgc 264

<210> 40

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 40

accacgtct gcgttgctgc c 21

<210> 41

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 41

gagaatatgc tggagagg 18

<210> 42

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 42

aggaatgcac taggattcgc gcgg 24

<210> 43

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 43

ggccccaag gcaaggacaa agcagctgtc agggaacctc cgccg 45

<210> 44  
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<212> DNA  
<213> Homo sapiens

<400> 44  
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atgagaacca aaaaacagct gtcgcaaac accgactctg tcgtgcctt 2000  
gatctgaac ttccagcctc cagaactatg agaaataaaa ttctggtgt 2050  
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<211> 359

<212> PRT

<213> Homo sapiens

<400> 45

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Leu Gly Val Leu Trp Val Ala Gln Met Leu Leu Ala Ala Ser Phe  
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Glu Thr Leu Gln Cys Glu Gly Pro Val Cys Thr Glu Glu Ser Ser  
35 40 45

Cys His Thr Glu Asp Asp Leu Thr Asp Ala Arg Glu Ala Gly Phe  
50 55 60

Gln Val Lys Ala Tyr Thr Phe Ser Glu Pro Phe His Leu Ile Val  
65 70 75

Ser Tyr Asp Trp Leu Ile Leu Gln Gly Pro Ala Lys Pro Val Phe  
80 85 90

Glu Gly Asp Leu Leu Val Leu Arg Cys Gln Ala Trp Gln Asp Trp  
95 100 105

Pro Leu Thr Gln Val Thr Phe Tyr Arg Asp Gly Ser Ala Leu Gly  
110 115 120

Pro Pro Gly Pro Asn Arg Glu Phe Ser Ile Thr Val Val Gln Lys  
125 130 135

Ala Asp Ser Gly His Tyr His Cys Ser Gly Ile Phe Gln Ser Pro  
140 145 150

Gly Pro Gly Ile Pro Glu Thr Ala Ser Val Val Ala Ile Thr Val  
155 160 165

Gln Glu Leu Phe Pro Ala Pro Ile Leu Arg Ala Val Pro Ser Ala  
170 175 180

Glu Pro Gln Ala Gly Ser Pro Met Thr Leu Ser Cys Gln Thr Lys  
185 190 195

Leu Pro Leu Gln Arg Ser Ala Ala Arg Leu Leu Phe Ser Phe Tyr



200	205	210
Lys Asp Gly Arg Ile Val Gln Ser Arg Gly Leu Ser Ser Glu Phe		
215	220	225
Gln Ile Pro Thr Ala Ser Glu Asp His Ser Gly Ser Tyr Trp Cys		
230	235	240
Glu Ala Ala Thr Glu Asp Asn Gln Val Trp Lys Gln Ser Pro Gln		
245	250	255
Leu Glu Ile Arg Val Gln Gly Ala Ser Ser Ser Ala Ala Pro Pro		
260	265	270
Thr Leu Asn Pro Ala Pro Gln Lys Ser Ala Ala Pro Gly Thr Ala		
275	280	285
Pro Glu Glu Ala Pro Gly Pro Leu Pro Pro Pro Pro Thr Pro Ser		
290	295	300
Ser Glu Asp Pro Gly Phe Ser Ser Pro Leu Gly Met Pro Asp Pro		
305	310	315
His Leu Tyr His Gln Met Gly Leu Leu Leu Lys His Met Gln Asp		
320	325	330
Val Arg Val Leu Leu Gly His Leu Leu Met Glu Leu Arg Glu Leu		
335	340	345
Ser Gly His Gln Lys Pro Gly Thr Thr Lys Ala Thr Ala Glu		
350	355	

<210> 46

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 46

tgggctgtgt cctcatgg 18

<210> 47

<211> 18

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 47  
ttccagcgc caattctc 18

<210> 48  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 48  
agttcttgga ctgtgatagc cac 23

<210> 49  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 49  
aaacttggt gtcctcagtg gctg 24

<210> 50  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 50  
gtgagggacc tgtctgcact gaggagagca gtgccacac ggagg 45

<210> 51  
<211> 2181  
<212> DNA

<213> Homo sapiens

<400> 51

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gcacctaaca gtggacactt atggcctcc catcctggaa gtgccagaga 200  
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tggtgctcaa taaatatcta atcataacag c 2181

<210> 52  
<211> 321  
<212> PRT  
<213> Homo sapiens

<400> 52  
Met Gly Ile Leu Leu Gly Leu Leu Leu Leu Gly His Leu Thr Val  
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Asp Thr Tyr Gly Arg Pro Ile Leu Glu Val Pro Glu Ser Val Thr  
20 25 30

Gly Pro Trp Lys Gly Asp Val Asn Leu Pro Cys Thr Tyr Asp Pro  
35 40 45

Leu Gln Gly Tyr Thr Gln Val Leu Val Lys Trp Leu Val Gln Arg  
50 55 60

Gly Ser Asp Pro Val Thr Ile Phe Leu Arg Asp Ser Ser Gly Asp  
65 70 75

His Ile Gln Gln Ala Lys Tyr Gln Gly Arg Leu His Val Ser His  
80 85 90

Lys Val Pro Gly Asp Val Ser Leu Gln Leu Ser Thr Leu Glu Met  
95 100 105

Asp Asp Arg Ser His Tyr Thr Cys Glu Val Thr Trp Gln Thr Pro  
110 115 120

Asp Gly Asn Gln Val Val Arg Asp Lys Ile Thr Glu Leu Arg Val  
125 130 135

Gln Lys Leu Ser Val Ser Lys Pro Thr Val Thr Thr Gly Ser Gly  
140 145 150

Tyr Gly Phe Thr Val Pro Gln Gly Met Arg Ile Ser Leu Gln Cys  
155 160 165

Gln Ala Arg Gly Ser Pro Pro Ile Ser Tyr Ile Trp Tyr Lys Gln  
170 175 180

Gln Thr Asn Asn Gln Glu Pro Ile Lys Val Ala Thr Leu Ser Thr  
185 190 195

Leu Leu Phe Lys Pro Ala Val Ile Ala Asp Ser Gly Ser Tyr Phe  
200 205 210

Cys Thr Ala Lys Gly Gln Val Gly Ser Glu Gln His Ser Asp Ile  
215 220 225

Val Lys Phe Val Val Lys Asp Ser Ser Lys Leu Leu Lys Thr Lys  
230 235 240

Thr Glu Ala Pro Thr Thr Met Thr Tyr Pro Leu Lys Ala Thr Ser  
245 250 255

Thr Val Lys Gln Ser Trp Asp Trp Thr Thr Asp Met Asp Gly Tyr  
260 265 270

Leu Gly Glu Thr Ser Ala Gly Pro Gly Lys Ser Leu Pro Val Phe  
275 280 285

Ala Ile Ile Leu Ile Ile Ser Leu Cys Cys Met Val Val Phe Thr  
290 295 300

Met Ala Tyr Ile Met Leu Cys Arg Lys Thr Ser Gln Gln Glu His  
305 310 315

Val Tyr Glu Ala Ala Arg  
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<210> 53

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 53

tatccctcca attgagcacc ctgg 24

<210> 54

<211> 21

<212> DNA

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<223> Synthetic oligonucleotide probe

<400> 54  
gtcgaagac atccaacaa g 21

<210> 55  
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<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 55  
cttcacaatg tcgctgtgct gctc 24

<210> 56  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 56  
agccaaatcc agcagctggc ttac 24

<210> 57  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 57  
tggatgaccg gagccactac acgtgtgaag tcacctggca gactcctgat 50

<210> 58  
<211> 2458  
<212> DNA  
<213> Homo sapiens

<400> 58  
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<210> 59

<211> 373

<212> PRT

<213> Homo sapiens

<400> 59

Met Ser Leu Leu Leu Leu Leu Leu Val Ser Tyr Tyr Val Gly

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Thr Leu Gly Thr His Thr Glu Ile Lys Arg Val Ala Glu Glu Lys

20 25 30

Val Thr Leu Pro Cys His His Gln Leu Gly Leu Pro Glu Lys Asp

35 40 45

Thr Leu Asp Ile Glu Trp Leu Leu Thr Asp Asn Glu Gly Asn Gln

50 55 60

Lys Val Val Ile Thr Tyr Ser Ser Arg His Val Tyr Asn Asn Leu

65 70 75

Thr Glu Glu Gln Lys Gly Arg Val Ala Phe Ala Ser Asn Phe Leu

80 85 90

Ala Gly Asp Ala Ser Leu Gln Ile Glu Pro Leu Lys Pro Ser Asp

95 100 105

Glu Gly Arg Tyr Thr Cys Lys Val Lys Asn Ser Gly Arg Tyr Val

110 115 120

Trp Ser His Val Ile Leu Lys Val Leu Val Arg Pro Ser Lys Pro

125 130 135

Lys Cys Glu Leu Glu Gly Glu Leu Thr Glu Gly Ser Asp Leu Thr

140 145 150

Leu Gln Cys Glu Ser Ser Ser Gly Thr Glu Pro Ile Val Tyr Tyr

155 160 165

Trp Gln Arg Ile Arg Glu Lys Glu Gly Glu Asp Glu Arg Leu Pro

170 175 180

Pro Lys Ser Arg Ile Asp Tyr Asn His Pro Gly Arg Val Leu Leu  
185 190 195

Gln Asn Leu Thr Met Ser Tyr Ser Gly Leu Tyr Gln Cys Thr Ala  
200 205 210

Gly Asn Glu Ala Gly Lys Glu Ser Cys Val Val Arg Val Thr Val  
215 220 225

Gln Tyr Val Gln Ser Ile Gly Met Val Ala Gly Ala Val Thr Gly  
230 235 240

Ile Val Ala Gly Ala Leu Leu Ile Phe Leu Leu Val Trp Leu Leu  
245 250 255

Ile Arg Arg Lys Asp Lys Glu Arg Tyr Glu Glu Glu Glu Arg Pro  
260 265 270

Asn Glu Ile Arg Glu Asp Ala Glu Ala Pro Lys Ala Arg Leu Val  
275 280 285

Lys Pro Ser Ser Ser Ser Ser Gly Ser Arg Ser Ser Arg Ser Gly  
290 295 300

Ser Ser Ser Thr Arg Ser Thr Ala Asn Ser Ala Ser Arg Ser Gln  
305 310 315

Arg Thr Leu Ser Thr Asp Ala Ala Pro Gln Pro Gly Leu Ala Thr  
320 325 330

Gln Ala Tyr Ser Leu Val Gly Pro Glu Val Arg Gly Ser Glu Pro  
335 340 345

Lys Lys Val His His Ala Asn Leu Thr Lys Ala Glu Thr Thr Pro  
350 355 360

Ser Met Ile Pro Ser Gln Ser Arg Ala Phe Gln Thr Val  
365 370

<210> 60

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 60

ccagtgcaca gcaggcaacg aagc 24

<210> 61

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 61

actaggctgt atgcctgggt gggc 24

<210> 62

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 62

gtatgtacaa agcatcggca tggttgcagg agcagtgaca ggc 43

<210> 63

<211> 3534

<212> DNA

<213> Homo sapiens

<400> 63

gtcgttcctt tgctctctcg cgcccagtc tctccctgg ttctctcag 50

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<210> 64

<211> 655

<212> PRT

<213> Homo sapiens

<400> 64

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Lys Ala Ser Asn Leu Ile Gly Thr Tyr Arg His Val Asp Arg Ala			
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Thr Gly Gln Val Leu Thr Cys Asp Lys Cys Pro Ala Gly Thr Tyr			
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Val Ser Glu His Cys Thr Asn Thr Ser Leu Arg Val Cys Ser Ser			
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Cys Pro Val Gly Thr Phe Thr Arg His Glu Asn Gly Ile Glu Lys			
95	100	105	
Cys His Asp Cys Ser Gln Pro Cys Pro Trp Pro Met Ile Glu Lys			
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Leu Pro Cys Ala Ala Leu Thr Asp Arg Glu Cys Thr Cys Pro Pro			
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Gly Met Phe Gln Ser Asn Ala Thr Cys Ala Pro His Thr Val Cys			
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Pro Val Gly Trp Gly Val Arg Lys Lys Gly Thr Glu Thr Glu Asp			
155	160	165	
Val Arg Cys Lys Gln Cys Ala Arg Gly Thr Phe Ser Asp Val Pro			
170	175	180	
Ser Ser Val Met Lys Cys Lys Ala Tyr Thr Asp Cys Leu Ser Gln			
185	190	195	
Asn Leu Val Val Ile Lys Pro Gly Thr Lys Glu Thr Asp Asn Val			
200	205	210	
Cys Gly Thr Leu Pro Ser Phe Ser Ser Ser Thr Ser Pro Ser Pro			
215	220	225	
Gly Thr Ala Ile Phe Pro Arg Pro Glu His Met Glu Thr His Glu			



230	235	240
Val Pro Ser Ser Thr Tyr Val Pro Lys Gly Met Asn Ser Thr Glu		
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Ser Asn Ser Ser Ala Ser Val Arg Pro Lys Val Leu Ser Ser Ile		
260	265	270
Gln Glu Gly Thr Val Pro Asp Asn Thr Ser Ser Ala Arg Gly Lys		
275	280	285
Glu Asp Val Asn Lys Thr Leu Pro Asn Leu Gln Val Val Asn His		
290	295	300
Gln Gln Gly Pro His His Arg His Ile Leu Lys Leu Leu Pro Ser		
305	310	315
Met Glu Ala Thr Gly Gly Glu Lys Ser Ser Thr Pro Ile Lys Gly		
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Pro Lys Arg Gly His Pro Arg Gln Asn Leu His Lys His Phe Asp		
335	340	345
Ile Asn Glu His Leu Pro Trp Met Ile Val Leu Phe Leu Leu Leu		
350	355	360
Val Leu Val Val Ile Val Val Cys Ser Ile Arg Lys Ser Ser Arg		
365	370	375
Thr Leu Lys Lys Gly Pro Arg Gln Asp Pro Ser Ala Ile Val Glu		
380	385	390
Lys Ala Gly Leu Lys Lys Ser Met Thr Pro Thr Gln Asn Arg Glu		
395	400	405
Lys Trp Ile Tyr Tyr Cys Asn Gly His Gly Ile Asp Ile Leu Lys		
410	415	420
Leu Val Ala Ala Gln Val Gly Ser Gln Trp Lys Asp Ile Tyr Gln		
425	430	435
Phe Leu Cys Asn Ala Ser Glu Arg Glu Val Ala Ala Phe Ser Asn		
440	445	450
Gly Tyr Thr Ala Asp His Glu Arg Ala Tyr Ala Ala Leu Gln His		

455	460	465
Trp Thr Ile Arg Gly Pro Glu Ala Ser Leu Ala Gln Leu Ile Ser		
470	475	480
Ala Leu Arg Gln His Arg Arg Asn Asp Val Val Glu Lys Ile Arg		
485	490	495
Gly Leu Met Glu Asp Thr Thr Gln Leu Glu Thr Asp Lys Leu Ala		
500	505	510
Leu Pro Met Ser Pro Ser Pro Leu Ser Pro Ser Pro Ile Pro Ser		
515	520	525
Pro Asn Ala Lys Leu Glu Asn Ser Ala Leu Leu Thr Val Glu Pro		
530	535	540
Ser Pro Gln Asp Lys Asn Lys Gly Phe Phe Val Asp Glu Ser Glu		
545	550	555
Pro Leu Leu Arg Cys Asp Ser Thr Ser Ser Gly Ser Ser Ala Leu		
560	565	570
Ser Arg Asn Gly Ser Phe Ile Thr Lys Glu Lys Lys Asp Thr Val		
575	580	585
Leu Arg Gln Val Arg Leu Asp Pro Cys Asp Leu Gln Pro Ile Phe		
590	595	600
Asp Asp Met Leu His Phe Leu Asn Pro Glu Glu Leu Arg Val Ile		
605	610	615
Glu Glu Ile Pro Gln Ala Glu Asp Lys Leu Asp Arg Leu Phe Glu		
620	625	630
Ile Ile Gly Val Lys Ser Gln Glu Ala Ser Gln Thr Leu Leu Asp		
635	640	645
Ser Val Tyr Ser His Leu Pro Asp Leu Leu		
650	655	

<210> 65

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 65

gtagcagtgc acatggggtg ttgg 24

<210> 66

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 66

accgcacatc ctcaagtctc gtcc 24

<210> 67

<211> 50

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 67

acgatgatcg cgggctccct tctcctgctt ggattcctta gcaccaccac 50

<210> 68

<211> 2412

<212> DNA

<213> Homo sapiens

<400> 68

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<210> 69

<211> 453

<212> PRT

<213> Homo sapiens

<400> 69

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20 25 30

Pro Asp Ala Asp Ala Val Ala Ala Gln Ile Leu Ser Leu Leu Pro  
35 40 45

Leu Lys Phe Phe Pro Ile Ile Val Ile Gly Ile Ile Ala Leu Ile  
50 55 60

Leu Ala Leu Ala Ile Gly Leu Gly Ile His Phe Asp Cys Ser Gly  
65 70 75

Lys Tyr Arg Cys Arg Ser Ser Phe Lys Cys Ile Glu Leu Ile Ala  
80 85 90

Arg Cys Asp Gly Val Ser Asp Cys Lys Asp Gly Glu Asp Glu Tyr  
95 100 105

Arg Cys Val Arg Val Gly Gly Gln Asn Ala Val Leu Gln Val Phe  
110 115 120

Thr Ala Ala Ser Trp Lys Thr Met Cys Ser Asp Asp Trp Lys Gly  
125 130 135

His Tyr Ala Asn Val Ala Cys Ala Gln Leu Gly Phe Pro Ser Tyr  
140 145 150

Val Ser Ser Asp Asn Leu Arg Val Ser Ser Leu Glu Gly Gln Phe  
155 160 165

Arg Glu Glu Phe Val Ser Ile Asp His Leu Leu Pro Asp Asp Lys  
170 175 180

Val Thr Ala Leu His His Ser Val Tyr Val Arg Glu Gly Cys Ala  
185 190 195

Ser Gly His Val Val Thr Leu Gln Cys Thr Ala Cys Gly His Arg  
200 205 210

Arg Gly Tyr Ser Ser Arg Ile Val Gly Gly Asn Met Ser Leu Leu  
215 220 225

Ser Gln Trp Pro Trp Gln Ala Ser Leu Gln Phe Gln Gly Tyr His  
230 235 240

Leu Cys Gly Gly Ser Val Ile Thr Pro Leu Trp Ile Ile Thr Ala  
245 250 255

Ala His Cys Val Tyr Asp Leu Tyr Leu Pro Lys Ser Trp Thr Ile  
260 265 270

Gln Val Gly Leu Val Ser Leu Leu Asp Asn Pro Ala Pro Ser His  
275 280 285

Leu Val Glu Lys Ile Val Tyr His Ser Lys Tyr Lys Pro Lys Arg  
290 295 300

Leu Gly Asn Asp Ile Ala Leu Met Lys Leu Ala Gly Pro Leu Thr  
305 310 315

Phe Asn Glu Met Ile Gln Pro Val Cys Leu Pro Asn Ser Glu Glu  
320 325 330

Asn Phe Pro Asp Gly Lys Val Cys Trp Thr Ser Gly Trp Gly Ala  
335 340 345

Thr Glu Asp Gly Gly Asp Ala Ser Pro Val Leu Asn His Ala Ala  
350 355 360

Val Pro Leu Ile Ser Asn Lys Ile Cys Asn His Arg Asp Val Tyr  
365 370 375

Gly Gly Ile Ile Ser Pro Ser Met Leu Cys Ala Gly Tyr Leu Thr  
380 385 390

Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val  
395 400 405

Cys Gln Glu Arg Arg Leu Trp Lys Leu Val Gly Ala Thr Ser Phe  
410 415 420

Gly Ile Gly Cys Ala Glu Val Asn Lys Pro Gly Val Tyr Thr Arg  
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Val Thr Ser Phe Leu Asp Trp Ile His Glu Gln Met Glu Arg Asp  
440 445 450

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<210> 70

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 70

tgacatcgcc cttatgaagc tggc 24

<210> 71

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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 72

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<212> DNA

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<400> 72

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<211> 3305

<212> DNA

<213> Homo sapiens

<400> 73

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caacccttca tttaacaagt aagaatgta aaaagtgaaa acaatgtaag 3250  
agcctaactc catccccctg ggccattact gcataaata gagtgcattt 3300  
gaaat 3305

<210> 74

<211> 735

<212> PRT

<213> Homo sapiens

<400> 74

Met Ala Ala Arg Pro Leu Pro Val Ser Pro Ala Arg Ala Leu Leu

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Leu Ala Leu Ala Gly Ala Leu Leu Ala Pro Cys Glu Ala Arg Gly			
20	25	30	
Val Ser Leu Trp Asn Gln Gly Arg Ala Asp Glu Val Val Ser Ala			
35	40	45	
Ser Val Arg Ser Gly Asp Leu Trp Ile Pro Val Lys Ser Phe Asp			
50	55	60	
Ser Lys Asn His Pro Glu Val Leu Asn Ile Arg Leu Gln Arg Glu			
65	70	75	
Ser Lys Glu Leu Ile Ile Asn Leu Glu Arg Asn Glu Gly Leu Ile			
80	85	90	
Ala Ser Ser Phe Thr Glu Thr His Tyr Leu Gln Asp Gly Thr Asp			
95	100	105	
Val Ser Leu Ala Arg Asn Tyr Thr Gly His Cys Tyr Tyr His Gly			
110	115	120	
His Val Arg Gly Tyr Ser Asp Ser Ala Val Ser Leu Ser Thr Cys			
125	130	135	
Ser Gly Leu Arg Gly Leu Ile Val Phe Glu Asn Glu Ser Tyr Val			
140	145	150	
Leu Glu Pro Met Lys Ser Ala Thr Asn Arg Tyr Lys Leu Phe Pro			
155	160	165	
Ala Lys Lys Leu Lys Ser Val Arg Gly Ser Cys Gly Ser His His			
170	175	180	
Asn Thr Pro Asn Leu Ala Ala Lys Asn Val Phe Pro Pro Pro Ser			
185	190	195	
Gln Thr Trp Ala Arg Arg His Lys Arg Glu Thr Leu Lys Ala Thr			
200	205	210	
Lys Tyr Val Glu Leu Val Ile Val Ala Asp Asn Arg Glu Phe Gln			
215	220	225	
Arg Gln Gly Lys Asp Leu Glu Lys Val Lys Gln Arg Leu Ile Glu			

230	235	240
Ile Ala Asn His Val Asp Lys Phe Tyr Arg Pro Leu Asn Ile Arg		
245	250	255
Ile Val Leu Val Gly Val Glu Val Trp Asn Asp Met Asp Lys Cys		
260	265	270
Ser Val Ser Gln Asp Pro Phe Thr Ser Leu His Glu Phe Leu Asp		
275	280	285
Trp Arg Lys Met Lys Leu Leu Pro Arg Lys Ser His Asp Asn Ala		
290	295	300
Gln Leu Val Ser Gly Val Tyr Phe Gln Gly Thr Thr Ile Gly Met		
305	310	315
Ala Pro Ile Met Ser Met Cys Thr Ala Asp Gln Ser Gly Gly Ile		
320	325	330
Val Met Asp His Ser Asp Asn Pro Leu Gly Ala Ala Val Thr Leu		
335	340	345
Ala His Glu Leu Gly His Asn Phe Gly Met Asn His Asp Thr Leu		
350	355	360
Asp Arg Gly Cys Ser Cys Gln Met Ala Val Glu Lys Gly Gly Cys		
365	370	375
Ile Met Asn Ala Ser Thr Gly Tyr Pro Phe Pro Met Val Phe Ser		
380	385	390
Ser Cys Ser Arg Lys Asp Leu Glu Thr Ser Leu Glu Lys Gly Met		
395	400	405
Gly Val Cys Leu Phe Asn Leu Pro Glu Val Arg Glu Ser Phe Gly		
410	415	420
Gly Gln Lys Cys Gly Asn Arg Phe Val Glu Glu Gly Glu Glu Cys		
425	430	435
Asp Cys Gly Glu Pro Glu Glu Cys Met Asn Arg Cys Cys Asn Ala		
440	445	450
Thr Thr Cys Thr Leu Lys Pro Asp Ala Val Cys Ala His Gly Leu		

455	460	465
Cys Cys Glu Asp Cys Gln Leu Lys Pro Ala Gly Thr Ala Cys Arg		
470	475	480
Asp Ser Ser Asn Ser Cys Asp Leu Pro Glu Phe Cys Thr Gly Ala		
485	490	495
Ser Pro His Cys Pro Ala Asn Val Tyr Leu His Asp Gly His Ser		
500	505	510
Cys Gln Asp Val Asp Gly Tyr Cys Tyr Asn Gly Ile Cys Gln Thr		
515	520	525
His Glu Gln Gln Cys Val Thr Leu Trp Gly Pro Gly Ala Lys Pro		
530	535	540
Ala Pro Gly Ile Cys Phe Glu Arg Val Asn Ser Ala Gly Asp Pro		
545	550	555
Tyr Gly Asn Cys Gly Lys Val Ser Lys Ser Ser Phe Ala Lys Cys		
560	565	570
Glu Met Arg Asp Ala Lys Cys Gly Lys Ile Gln Cys Gln Gly Gly		
575	580	585
Ala Ser Arg Pro Val Ile Gly Thr Asn Ala Val Ser Ile Glu Thr		
590	595	600
Asn Ile Pro Leu Gln Gln Gly Gly Arg Ile Leu Cys Arg Gly Thr		
605	610	615
His Val Tyr Leu Gly Asp Asp Met Pro Asp Pro Gly Leu Val Leu		
620	625	630
Ala Gly Thr Lys Cys Ala Asp Gly Lys Ile Cys Leu Asn Arg Gln		
635	640	645
Cys Gln Asn Ile Ser Val Phe Gly Val His Glu Cys Ala Met Gln		
650	655	660
Cys His Gly Arg Gly Val Cys Asn Asn Arg Lys Asn Cys His Cys		
665	670	675
Glu Ala His Trp Ala Pro Pro Phe Cys Asp Lys Phe Gly Phe Gly		

680	685	690
Gly Ser Thr Asp Ser Gly Pro Ile Arg Gln Ala Glu Ala Arg Gln		
695	700	705
Glu Ala Ala Glu Ser Asn Arg Glu Arg Gly Gln Gly Gln Glu Pro		
710	715	720
Val Gly Ser Gln Glu His Ala Ser Thr Ala Ser Leu Thr Leu Ile		
725	730	735

<210> 75

<211> 483

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 30, 94, 143, 156, 163, 179, 193, 369, 371, 381, 390, 473

<223> unknown base

<400> 75

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ctgacaacga aaacaaaaca gtttggggg ttcaggaggg gaantccagc 100

ctaccagga agttgcaga aacagtcaa ggaagggcag ganttcctgg 150

ttgagnttt tgntaaaaca tggacatgnt tcagtgtgc tentgagaga 200

gtagcagggtt accactttg gcaggcccca gccctgcagc aaggaggaag 250

aggactcaaa agttggcct ttcactgagc ctccacagca gtgggggaga 300

agcaagggtt gggcccagtg tccccttcc ccagtgcac ctgccttg 350

gcagccctga taactggtnt ntggctgcaa nttaatgctn tgatatggct 400

tttagcattt attatatgaa aatagcaggg ttttagttt taatttatca 450

gagaccctgc cacccattcc atntccatcc aag 483

<210> 76

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 76

gtctcagcac gtgttctggt ctcaggg 27

<210> 77

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 77

catgagcatg tgcacggc 18

<210> 78

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 78

tacctgcacg atgggcac 18

<210> 79

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 79

cactgggcac ctccttc 18

<210> 80

<211> 26

<212> DNA

<213> Artificial Sequence



<220>

<223> Synthetic oligonucleotide probe

<400> 80

ctccaggctg gtctccaagt ccttcc 26

<210> 81

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 81

tcctgttgg actctgcagc ttcc 24

<210> 82

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 82

cttcgctggg aagagtttg 19

<210> 83

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 83

gtgcaaccaa cagatacaaa ctcttcccag cgaagaagct gaaaagcgtc 50

<210> 84

<211> 1714

<212> DNA

<213> Homo sapiens

<400> 84

catcctgcaa catggtgaaa ccacgcctgg ctaattttgt tgtattttg 50  
gtagagatgg gatttcaccg tgtagccag gattgtctca atctgacctc 100  
atgatctgcc cgctcggcc tcccaaagtg ctgggattac aggcgagtgc 150  
aaccacaccc ggccacaaac ttttaagaa gttaatgaaa ccatacctt 200  
tacatttta atgacaggaa aatgctcaca ataattgta acccaaaatt 250  
ctggatacaa aagtacaatc ttactgtgt aaatacatgt atatgtacta 300  
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ttctcatacc ctgtgctaac aactttaac aaaaatttg catcacttt 400  
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<210> 85

<211> 67

<212> PRT

<213> Homo sapiens

<400> 85

Met Gly Lys Gly Met Val Ala Met Leu Ile Leu Gly Leu Leu Leu  
 1 5 10 15

Leu Ala Leu Leu Leu Pro Val Gln Val Ser Ser Phe Val Pro Leu  
 20 25 30

Thr Ser Met Pro Glu Ala Thr Ala Ala Glu Thr Thr Lys Pro Ser  
 35 40 45

Asn Ser Ala Leu Gln Pro Thr Ala Gly Leu Leu Val Val Leu Leu  
 50 55 60

Ala Leu Leu His Leu Tyr His  
 65

<210> 86  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 86  
acgggcacac tggatccaa atg 23

<210> 87  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 87  
ggtagagatg tagaaggga agcaagacc 29

<210> 88  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 88  
gctccctacc cgtgcagggt tcttcattg ttctttaac cagtatgccg 50

<210> 89  
<211> 2956  
<212> DNA  
<213> Homo sapiens

<400> 89  
ggcgcggcga gagcgcgcc agccccgccg cgatgccgc gcgccagga 50  
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gctgctgctg ggccatggcg gcggcgggcg ctggggcgcc cgggccagg 150

aggcggcggc ggcggcggcg gacgggcccc ccgcggcaga cggcgaggac 200  
ggacaggacc cgcacagcaa gcacctgtac acggccgaca tgttcacga 250  
cgggatccag agcgcgcgcg acttcgtcat gttcttcgcg ccctgggtg 300  
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cacaacttca gctttgcatc acgagtcttg tattccaaga aaatcaaagt 2900

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ttttaa 2956

<210> 90

<211> 432

<212> PRT

<213> Homo sapiens

<400> 90

Met Pro Ala Arg Pro Gly Arg Leu Leu Pro Leu Leu Ala Arg Pro  
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Ala Ala Leu Thr Ala Leu Leu Leu Leu Leu Gly His Gly Gly  
20 25 30

Gly Gly Arg Trp Gly Ala Arg Ala Gln Glu Ala Ala Ala Ala  
35 40 45

Ala Asp Gly Pro Pro Ala Ala Asp Gly Glu Asp Gly Gln Asp Pro  
50 55 60

His Ser Lys His Leu Tyr Thr Ala Asp Met Phe Thr His Gly Ile  
65 70 75

Gln Ser Ala Ala His Phe Val Met Phe Phe Ala Pro Trp Cys Gly  
80 85 90

His Cys Gln Arg Leu Gln Pro Thr Trp Asn Asp Leu Gly Asp Lys  
95 100 105

Tyr Asn Ser Met Glu Asp Ala Lys Val Tyr Val Ala Lys Val Asp  
110 115 120

Cys Thr Ala His Ser Asp Val Cys Ser Ala Gln Gly Val Arg Gly  
125 130 135

Tyr Pro Thr Leu Lys Leu Phe Lys Pro Gly Gln Glu Ala Val Lys  
140 145 150

Tyr Gln Gly Pro Arg Asp Phe Gln Thr Leu Glu Asn Trp Met Leu  
155 160 165

Gln Thr Leu Asn Glu Glu Pro Val Thr Pro Glu Pro Glu Val Glu  
170 175 180

Pro Pro Ser Ala Pro Glu Leu Lys Gln Gly Leu Tyr Glu Leu Ser  
185 190 195

Ala Ser Asn Phe Glu Leu His Val Ala Gln Gly Asp His Phe Ile  
200 205 210

Lys Phe Phe Ala Pro Trp Cys Gly His Cys Lys Ala Leu Ala Pro  
215 220 225

Thr Trp Glu Gln Leu Ala Leu Gly Leu Glu His Ser Glu Thr Val  
230 235 240

Lys Ile Gly Lys Val Asp Cys Thr Gln His Tyr Glu Leu Cys Ser  
245 250 255

Gly Asn Gln Val Arg Gly Tyr Pro Thr Leu Leu Trp Phe Arg Asp  
260 265 270

Gly Lys Lys Val Asp Gln Tyr Lys Gly Lys Arg Asp Leu Glu Ser  
275 280 285

Leu Arg Glu Tyr Val Glu Ser Gln Leu Gln Arg Thr Glu Thr Gly  
290 295 300

Ala Thr Glu Thr Val Thr Pro Ser Glu Ala Pro Val Leu Ala Ala  
305 310 315



Glu Pro Glu Ala Asp Lys Gly Thr Val Leu Ala Leu Thr Glu Asn  
320 325 330

Asn Phe Asp Asp Thr Ile Ala Glu Gly Ile Thr Phe Ile Lys Phe  
335 340 345

Tyr Ala Pro Trp Cys Gly His Cys Lys Thr Leu Ala Pro Thr Trp  
350 355 360

Glu Glu Leu Ser Lys Lys Glu Phe Pro Gly Leu Ala Gly Val Lys  
365 370 375

Ile Ala Glu Val Asp Cys Thr Ala Glu Arg Asn Ile Cys Ser Lys  
380 385 390

Tyr Ser Val Arg Gly Tyr Pro Thr Leu Leu Leu Phe Arg Gly Gly  
395 400 405

Lys Lys Val Ser Glu His Ser Gly Gly Arg Asp Leu Asp Ser Leu  
410 415 420

His Arg Phe Val Leu Ser Gln Ala Lys Asp Glu Leu  
425 430

<210> 91

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 91

atgttcttcg cgccctggtg 20

<210> 92

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 92

ccaagccaac acactctaca g 21

<210> 93  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 93  
aagtggtcgc cttgtgcaac gtgc 24

<210> 94  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 94  
ggtcaaaggg gatatatcgc cac 23

<210> 95  
<211> 49  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 95  
gcatggaaga tgccaaagtc tatgtggcta aagtggactg cacggccca 49

<210> 96  
<211> 1016  
<212> DNA  
<213> Homo sapiens

<400> 96  
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aaaccaattt atcctcctgg tactatttct ttgcaaatt cagagtctgg 100

gtctggatat tgatagccgt cctaccgctg aagtctgtgc cacacacaca 150

atttcaccag gacccaaagg agatgatggt gaaaaaggag atccaggaga 200  
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 gagaactggg tgatatggga gatcagggca atattggcaa gactgggccc 300  
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 aaaaaaaaaa aaaaaa 1016

<210> 97

<211> 277

<212> PRT

<213> Homo sapiens

<400> 97

Met Asn Gly Phe Ala Ser Leu Leu Arg Arg Asn Gln Phe Ile Leu

1

5

10

15

Leu Val Leu Phe Leu Leu Gln Ile Gln Ser Leu Gly Leu Asp Ile  
20 25 30

Asp Ser Arg Pro Thr Ala Glu Val Cys Ala Thr His Thr Ile Ser  
35 40 45

Pro Gly Pro Lys Gly Asp Asp Gly Glu Lys Gly Asp Pro Gly Glu  
50 55 60

Glu Gly Lys His Gly Lys Val Gly Arg Met Gly Pro Lys Gly Ile  
65 70 75

Lys Gly Glu Leu Gly Asp Met Gly Asp Gln Gly Asn Ile Gly Lys  
80 85 90

Thr Gly Pro Ile Gly Lys Lys Gly Asp Lys Gly Glu Lys Gly Leu  
95 100 105

Leu Gly Ile Pro Gly Glu Lys Gly Lys Ala Gly Thr Val Cys Asp  
110 115 120

Cys Gly Arg Tyr Arg Lys Phe Val Gly Gln Leu Asp Ile Ser Ile  
125 130 135

Ala Arg Leu Lys Thr Ser Met Lys Phe Val Lys Asn Val Ile Ala  
140 145 150

Gly Ile Arg Glu Thr Glu Glu Lys Phe Tyr Tyr Ile Val Gln Glu  
155 160 165

Glu Lys Asn Tyr Arg Glu Ser Leu Thr His Cys Arg Ile Arg Gly  
170 175 180

Gly Met Leu Ala Met Pro Lys Asp Glu Ala Ala Asn Thr Leu Ile  
185 190 195

Ala Asp Tyr Val Ala Lys Ser Gly Phe Phe Arg Val Phe Ile Gly  
200 205 210

Val Asn Asp Leu Glu Arg Glu Gly Gln Tyr Met Ser Thr Asp Asn  
215 220 225

Thr Pro Leu Gln Asn Tyr Ser Asn Trp Asn Glu Gly Glu Pro Ser  
230 235 240

Asp Pro Tyr Gly His Glu Asp Cys Val Glu Met Leu Ser Ser Gly  
245 250 255

Arg Trp Asn Asp Thr Glu Cys His Leu Thr Met Tyr Phe Val Cys  
260 265 270

Glu Phe Ile Lys Lys Lys Lys  
275

<210> 98

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 98

cgctgactat gttgccaaga gtgg 24

<210> 99

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 99

gatgatggag gctccatacc tcag 24

<210> 100

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 100

gtgttcattg gcgtgaatga ccttgaaagg gagggacagt acatgttcac 50

<210> 101

<211> 2574

<212> DNA

<213> Homo sapiens

<400> 101

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gggcctgggt gggaatgggc gtgtgccagc gcacgcgcgc tccctggaag 150  
gagaagtctc agctagaacg agcggcccta ggttttcgga agggaggatc 200  
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gctccatggc tgccctctg ctgctgcccc tgctgctgtt gctaccgctg 300  
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<211> 730  
<212> PRT  
<213> Homo sapiens

<400> 102  
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35 40 45  
Gly Ser Met Ala Ala Leu Leu Leu Leu Pro Leu Leu Leu Leu Leu  
50 55 60  
Pro Leu Leu Leu Leu Lys Leu His Leu Trp Pro Gln Leu Arg Trp  
65 70 75  
Leu Pro Ala Asp Leu Ala Phe Ala Val Arg Ala Leu Cys Cys Lys  
80 85 90  
Arg Ala Leu Arg Ala Arg Ala Leu Ala Ala Ala Ala Asp Pro  
95 100 105  
Glu Gly Pro Glu Gly Gly Cys Ser Leu Ala Trp Arg Leu Ala Glu  
110 115 120



Leu Ala Gln Gln Arg Ala Ala His Thr Phe Leu Ile His Gly Ser  
125 130 135

Arg Arg Phe Ser Tyr Ser Glu Ala Glu Arg Glu Ser Asn Arg Ala  
140 145 150

Ala Arg Ala Phe Leu Arg Ala Leu Gly Trp Asp Trp Gly Pro Asp  
155 160 165

Gly Gly Asp Ser Gly Glu Gly Ser Ala Gly Glu Gly Glu Arg Ala  
170 175 180

Ala Pro Gly Ala Gly Asp Ala Ala Ala Gly Ser Gly Ala Glu Phe  
185 190 195

Ala Gly Gly Asp Gly Ala Ala Arg Gly Gly Gly Ala Ala Ala Pro  
200 205 210

Leu Ser Pro Gly Ala Thr Val Ala Leu Leu Leu Pro Ala Gly Pro  
215 220 225

Glu Phe Leu Trp Leu Trp Phe Gly Leu Ala Lys Ala Gly Leu Arg  
230 235 240

Thr Ala Phe Val Pro Thr Ala Leu Arg Arg Gly Pro Leu Leu His  
245 250 255

Cys Leu Arg Ser Cys Gly Ala Arg Ala Leu Val Leu Ala Pro Glu  
260 265 270

Phe Leu Glu Ser Leu Glu Pro Asp Leu Pro Ala Leu Arg Ala Met  
275 280 285

Gly Leu His Leu Trp Ala Ala Gly Pro Gly Thr His Pro Ala Gly  
290 295 300

Ile Ser Asp Leu Leu Ala Glu Val Ser Ala Glu Val Asp Gly Pro  
305 310 315

Val Pro Gly Tyr Leu Ser Ser Pro Gln Ser Ile Thr Asp Thr Cys  
320 325 330

Leu Tyr Ile Phe Thr Ser Gly Thr Thr Gly Leu Pro Lys Ala Ala  
335 340 345

Arg Ile Ser His Leu Lys Ile Leu Gln Cys Gln Gly Phe Tyr Gln  
350 355 360

Leu Cys Gly Val His Gln Glu Asp Val Ile Tyr Leu Ala Leu Pro  
365 370 375

Leu Tyr His Met Ser Gly Ser Leu Leu Gly Ile Val Gly Cys Met  
380 385 390

Gly Ile Gly Ala Thr Val Val Leu Lys Ser Lys Phe Ser Ala Gly  
395 400 405

Gln Phe Trp Glu Asp Cys Gln Gln His Arg Val Thr Val Phe Gln  
410 415 420

Tyr Ile Gly Glu Leu Cys Arg Tyr Leu Val Asn Gln Pro Pro Ser  
425 430 435

Lys Ala Glu Arg Gly His Lys Val Arg Leu Ala Val Gly Ser Gly  
440 445 450

Leu Arg Pro Asp Thr Trp Glu Arg Phe Val Arg Arg Phe Gly Pro  
455 460 465

Leu Gln Val Leu Glu Thr Tyr Gly Leu Thr Glu Gly Asn Val Ala  
470 475 480

Thr Ile Asn Tyr Thr Gly Gln Arg Gly Ala Val Gly Arg Ala Ser  
485 490 495

Trp Leu Tyr Lys His Ile Phe Pro Phe Ser Leu Ile Arg Tyr Asp  
500 505 510

Val Thr Thr Gly Glu Pro Ile Arg Asp Pro Gln Gly His Cys Met  
515 520 525

Ala Thr Ser Pro Gly Glu Pro Gly Leu Leu Val Ala Pro Val Ser  
530 535 540

Gln Gln Ser Pro Phe Leu Gly Tyr Ala Gly Gly Pro Glu Leu Ala  
545 550 555

Gln Gly Lys Leu Leu Lys Asp Val Phe Arg Pro Gly Asp Val Phe  
560 565 570

Phe Asn Thr Gly Asp Leu Leu Val Cys Asp Asp Gln Gly Phe Leu  
575 580 585

Arg Phe His Asp Arg Thr Gly Asp Thr Phe Arg Trp Lys Gly Glu  
590 595 600

Asn Val Ala Thr Thr Glu Val Ala Glu Val Phe Glu Ala Leu Asp  
605 610 615

Phe Leu Gln Glu Val Asn Val Tyr Gly Val Thr Val Pro Gly His  
620 625 630

Glu Gly Arg Ala Gly Met Ala Ala Leu Val Leu Arg Pro Pro His  
635 640 645

Ala Leu Asp Leu Met Gln Leu Tyr Thr His Val Ser Glu Asn Leu  
650 655 660

Pro Pro Tyr Ala Arg Pro Arg Phe Leu Arg Leu Gln Glu Ser Leu  
665 670 675

Ala Thr Thr Glu Thr Phe Lys Gln Gln Lys Val Arg Met Ala Asn  
680 685 690

Glu Gly Phe Asp Pro Ser Thr Leu Ser Asp Pro Leu Tyr Val Leu  
695 700 705

Asp Gln Ala Val Gly Ala Tyr Leu Pro Leu Thr Thr Ala Arg Tyr  
710 715 720

Ser Ala Leu Leu Ala Gly Asn Leu Arg Ile  
725 730

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<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 103

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<210> 104

<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 104  
ggagaatgtg gccacaac 18

<210> 105  
<211> 26  
<212> DNA  
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<220>  
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<400> 105  
gccctggcac agtgactcca tagacg 26

<210> 106  
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<220>  
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<400> 106  
atccactca gcggacac 18

<210> 107  
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<213> Artificial Sequence

<220>  
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<400> 107  
ccagtgccag gatacctctc ttccccccag agcataacag acacg 45

<210> 108  
<211> 2579

<212> DNA

<213> Homo sapiens

<400> 108

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acgcgcgcgc acacactcgc tctcgcttgc ccctctccct cccgggggag 150  
ccggcgcgcg ctcccacatt tgccgcacac tccggcgagc cgagcccgcga 200  
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accgtttcca tctgggggct agaggagcaa ggcagcagcc ttcccagcca 350  
gcccttggtg gcttgccatc gtccatctgg cttataaaag ttgctgagc 400  
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ttctacctt catttgcttt tatgtgcag aagtaaagga atctcacgtt 2550

gtgagggttt ttttttctc atttaaaat 2579

<210> 109

<211> 555

<212> PRT

<213> Homo sapiens

<400> 109

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Leu Leu Ser Leu Pro Ala Gly Ala Asp Val Lys Ala Arg Ser Cys  
20 25 30

Gly Glu Val Arg Gln Ala Tyr Gly Ala Lys Gly Phe Ser Leu Ala  
35 40 45

Asp Ile Pro Tyr Gln Glu Ile Ala Gly Glu His Leu Arg Ile Cys  
50 55 60

Pro Gln Glu Tyr Thr Cys Cys Thr Thr Glu Met Glu Asp Lys Leu  
65 70 75

Ser Gln Gln Ser Lys Leu Glu Phe Glu Asn Leu Val Glu Glu Thr  
80 85 90

Ser His Phe Val Arg Thr Thr Phe Val Ser Arg His Lys Lys Phe  
95 100 105

Asp Glu Phe Phe Arg Glu Leu Leu Glu Asn Ala Glu Lys Ser Leu  
110 115 120

Asn Asp Met Phe Val Arg Thr Tyr Gly Met Leu Tyr Met Gln Asn  
125 130 135

Ser Glu Val Phe Gln Asp Leu Phe Thr Glu Leu Lys Arg Tyr Tyr  
140 145 150

Thr Gly Gly Asn Val Asn Leu Glu Glu Met Leu Asn Asp Phe Trp  
155 160 165

Ala Arg Leu Leu Glu Arg Met Phe Gln Leu Ile Asn Pro Gln Tyr  
170 175 180

His Phe Ser Glu Asp Tyr Leu Glu Cys Val Ser Lys Tyr Thr Asp  
185 190 195

Gln Leu Lys Pro Phe Gly Asp Val Pro Arg Lys Leu Lys Ile Gln  
200 205 210

Val Thr Arg Ala Phe Ile Ala Ala Arg Thr Phe Val Gln Gly Leu  
215 220 225

Thr Val Gly Arg Glu Val Ala Asn Arg Val Ser Lys Val Ser Pro  
230 235 240

Thr Pro Gly Cys Ile Arg Ala Leu Met Lys Met Leu Tyr Cys Pro  
245 250 255

Tyr Cys Arg Gly Leu Pro Thr Val Arg Pro Cys Asn Asn Tyr Cys  
260 265 270

Leu Asn Val Met Lys Gly Cys Leu Ala Asn Gln Ala Asp Leu Asp  
275 280 285

Thr Glu Trp Asn Leu Phe Ile Asp Ala Met Leu Leu Val Ala Glu  
290 295 300

Arg Leu Glu Gly Pro Phe Asn Ile Glu Ser Val Met Asp Pro Ile  
305 310 315

Asp Val Lys Ile Ser Glu Ala Ile Met Asn Met Gln Glu Asn Ser  
320 325 330

Met Gln Val Ser Ala Lys Val Phe Gln Gly Cys Gly Gln Pro Lys  
335 340 345



Pro Ala Pro Ala Leu Arg Ser Ala Arg Ser Ala Pro Glu Asn Phe  
350 355 360

Asn Thr Arg Phe Arg Pro Tyr Asn Pro Glu Glu Arg Pro Thr Thr  
365 370 375

Ala Ala Gly Thr Ser Leu Asp Arg Leu Val Thr Asp Ile Lys Glu  
380 385 390

Lys Leu Lys Leu Ser Lys Lys Val Trp Ser Ala Leu Pro Tyr Thr  
395 400 405

Ile Cys Lys Asp Glu Ser Val Thr Ala Gly Thr Ser Asn Glu Glu  
410 415 420

Glu Cys Trp Asn Gly His Ser Lys Ala Arg Tyr Leu Pro Glu Ile  
425 430 435

Met Asn Asp Gly Leu Thr Asn Gln Ile Asn Asn Pro Glu Val Asp  
440 445 450

Val Asp Ile Thr Arg Pro Asp Thr Phe Ile Arg Gln Gln Ile Met  
455 460 465

Ala Leu Arg Val Met Thr Asn Lys Leu Lys Asn Ala Tyr Asn Gly  
470 475 480

Asn Asp Val Asn Phe Gln Asp Thr Ser Asp Glu Ser Ser Gly Ser  
485 490 495

Gly Ser Gly Ser Gly Cys Met Asp Asp Val Cys Pro Thr Glu Phe  
500 505 510

Glu Phe Val Thr Thr Glu Ala Pro Ala Val Asp Pro Asp Arg Arg  
515 520 525

Glu Val Asp Ser Ser Ala Ala Gln Arg Gly His Ser Leu Leu Ser  
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Trp Ser Leu Thr Cys Ile Val Leu Ala Leu Gln Arg Leu Cys Arg  
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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 110

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<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 112

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<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 112

gaatgctgga acgggcacag caaagccaga tacttgctg 40

<210> 113

<211> 4649

<212> DNA

<213> Homo sapiens

<400> 113

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<210> 114

<211> 515

<212> PRT

<213> Homo sapiens

<400> 114

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Ala Gly Phe Trp Ile Leu Cys Leu Leu Thr Tyr Gly Tyr Leu Ser			
35	40	45	
Trp Gly Gln Ala Leu Glu Glu Glu Glu Gly Ala Leu Leu Ala			
50	55	60	
Gln Ala Gly Glu Lys Leu Glu Pro Ser Thr Thr Ser Thr Ser Gln			
65	70	75	
Pro His Leu Ile Phe Ile Leu Ala Asp Asp Gln Gly Phe Arg Asp			
80	85	90	
Val Gly Tyr His Gly Ser Glu Ile Lys Thr Pro Thr Leu Asp Lys			
95	100	105	
Leu Ala Ala Glu Gly Val Lys Leu Glu Asn Tyr Tyr Val Gln Pro			
110	115	120	
Ile Cys Thr Pro Ser Arg Ser Gln Phe Ile Thr Gly Lys Tyr Gln			
125	130	135	
Ile His Thr Gly Leu Gln His Ser Ile Ile Arg Pro Thr Gln Pro			
140	145	150	
Asn Cys Leu Pro Leu Asp Asn Ala Thr Leu Pro Gln Lys Leu Lys			
155	160	165	
Glu Val Gly Tyr Ser Thr His Met Val Gly Lys Trp His Leu Gly			
170	175	180	
Phe Asn Arg Lys Glu Cys Met Pro Thr Arg Arg Gly Phe Asp Thr			
185	190	195	
Phe Phe Gly Ser Leu Leu Gly Ser Gly Asp Tyr Tyr Thr His Tyr			
200	205	210	
Lys Cys Asp Ser Pro Gly Met Cys Gly Tyr Asp Leu Tyr Glu Asn			
215	220	225	
Asp Asn Ala Ala Trp Asp Tyr Asp Asn Gly Ile Tyr Ser Thr Gln			

230 235 240

Met Tyr Thr Gln Arg Val Gln Gln Ile Leu Ala Ser His Asn Pro  
245 250 255

Thr Lys Pro Ile Phe Leu Tyr Thr Ala Tyr Gln Ala Val His Ser  
260 265 270

Pro Leu Gln Ala Pro Gly Arg Tyr Phe Glu His Tyr Arg Ser Ile  
275 280 285

Ile Asn Ile Asn Arg Arg Arg Tyr Ala Ala Met Leu Ser Cys Leu  
290 295 300

Asp Glu Ala Ile Asn Asn Val Thr Leu Ala Leu Lys Thr Tyr Gly  
305 310 315

Phe Tyr Asn Asn Ser Ile Ile Ile Tyr Ser Ser Asp Asn Gly Gly  
320 325 330

Gln Pro Thr Ala Gly Gly Ser Asn Trp Pro Leu Arg Gly Ser Lys  
335 340 345

Gly Thr Tyr Trp Glu Gly Gly Ile Arg Ala Val Gly Phe Val His  
350 355 360

Ser Pro Leu Leu Lys Asn Lys Gly Thr Val Cys Lys Glu Leu Val  
365 370 375

His Ile Thr Asp Trp Tyr Pro Thr Leu Ile Ser Leu Ala Glu Gly  
380 385 390

Gln Ile Asp Glu Asp Ile Gln Leu Asp Gly Tyr Asp Ile Trp Glu  
395 400 405

Thr Ile Ser Glu Gly Leu Arg Ser Pro Arg Val Asp Ile Leu His  
410 415 420

Asn Ile Asp Pro Tyr Thr Pro Arg Gln Lys Met Ala Pro Gly Gln  
425 430 435

Gln Ala Met Gly Ser Gly Thr Leu Gln Ser Ser Gln Pro Ser Glu  
440 445 450

Cys Ser Thr Gly Asn Cys Leu Gln Glu Ile Leu Ala Thr Ala Thr



455 460 465

Gly Ser Pro Leu Ser Leu Ser Ala Thr Trp Asp Arg Thr Gly Gly  
470 475 480

Thr Met Asn Gly Ser Pro Cys Gln Leu Ala Lys Val Tyr Gly Phe  
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Ser Thr Ser Gln Pro Thr His Met Arg Gly Trp Thr Tyr Leu Thr  
500 505 510

Gly Ile Gln Glu Ser  
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<210> 115  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 115  
cccaacccaa ctgtttacct ctgg 24

<210> 116  
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<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 116  
ctctctgagt gtacatctgt gtgg 24

<210> 117  
<211> 53  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

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<221> unsure  
<222> 33  
<223> unknown base

<400> 117  
gccaccctac ctcagaaact gaaggagggt ggntattcaa cgcatatggt 50  
  
cgg 53

<210> 118  
<211> 2260  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 2009, 2026, 2033, 2055, 2074, 2078, 2086  
<223> unknown base

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gggctcagga ggaggaagga ggacccgtgc gagaatgcct ctgccctgga 150  
  
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aacctgcagt caagatgtga atgagtgtg aatgaaacc cgccatgcc 450  
  
aacacagatg tgtgaataca cacggaagct acaagtgtt ttgcctcagt 500  
  
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<210> 119  
 <211> 338  
 <212> PRT  
 <213> Homo sapiens

<400> 119

Met Pro Leu Pro Trp Ser Leu Ala Leu Pro Leu Leu Ser Trp  
 1 5 10 15

Val Ala Gly Gly Phe Gly Asn Ala Ala Ser Ala Arg His His Gly  
 20 25 30

Leu Leu Ala Ser Ala Arg Gln Pro Gly Val Cys His Tyr Gly Thr  
 35 40 45

Lys Leu Ala Cys Cys Tyr Gly Trp Arg Arg Asn Ser Lys Gly Val  
 50 55 60

Cys Glu Ala Thr Cys Glu Pro Gly Cys Lys Phe Gly Glu Cys Val  
 65 70 75

Gly Pro Asn Lys Cys Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr  
 80 85 90

Cys Ser Gln Asp Val Asn Glu Cys Gly Met Lys Pro Arg Pro Cys

95	100	105
Gln His Arg Cys Val Asn Thr His Gly Ser Tyr Lys Cys Phe Cys		
110	115	120
Leu Ser Gly His Met Leu Met Pro Asp Ala Thr Cys Val Asn Ser		
125	130	135
Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys Glu Asp Thr		
140	145	150
Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu Arg Leu		
155	160	165
Ala Pro Asn Gly Arg Asp Cys Leu Asp Ile Asp Glu Cys Ala Ser		
170	175	180
Gly Lys Val Ile Cys Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe		
185	190	195
Gly Ser Tyr Tyr Cys Lys Cys His Ile Gly Phe Glu Leu Gln Tyr		
200	205	210
Ile Ser Gly Arg Tyr Asp Cys Ile Asp Ile Asn Glu Cys Thr Met		
215	220	225
Asp Ser His Thr Cys Ser His His Ala Asn Cys Phe Asn Thr Gln		
230	235	240
Gly Ser Phe Lys Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly		
245	250	255
Leu Arg Cys Ser Ala Ile Pro Glu Asn Ser Val Lys Glu Val Leu		
260	265	270
Arg Ala Pro Gly Thr Ile Lys Asp Arg Ile Lys Lys Leu Leu Ala		
275	280	285
His Lys Asn Ser Met Lys Lys Lys Ala Lys Ile Lys Asn Val Thr		
290	295	300
Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val Asn Leu Gln Pro		
305	310	315
Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly		

320

325

330

Gly Lys Lys Gly Asn Glu Glu Lys  
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<210> 120

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 120

cctcagtggc cacatgctca tg 22

<210> 121

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 121

ggctgcacgt atggctatcc atag 24

<210> 122

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 122

gataaactgt cagtacagct gtgaagacac agaagaaggg ccacagtgcc 50

<210> 123

<211> 1199

<212> DNA

<213> Homo sapiens

<400> 123

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ggccgagtgg cagggacgac gcccagaatg ggagctgact gatatggtgg 150  
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<210> 124

<211> 289

<212> PRT

<213> Homo sapiens

<400> 124

Met Val Val Trp Val Thr Gly Ala Ser Ser Gly Ile Gly Glu Glu

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Leu Ala Tyr Gln Leu Ser Lys Leu Gly Val Ser Leu Val Leu Ser

20 25 30

Ala Arg Arg Val His Glu Leu Glu Arg Val Lys Arg Arg Cys Leu

35 40 45

Glu Asn Gly Asn Leu Lys Glu Lys Asp Ile Leu Val Leu Pro Leu

50 55 60

Asp Leu Thr Asp Thr Gly Ser His Glu Ala Ala Thr Lys Ala Val

65 70 75

Leu Gln Glu Phe Gly Arg Ile Asp Ile Leu Val Asn Asn Gly Gly

80 85 90

Met Ser Gln Arg Ser Leu Cys Met Asp Thr Ser Leu Asp Val Tyr

95 100 105

Arg Lys Leu Ile Glu Leu Asn Tyr Leu Gly Thr Val Ser Leu Thr

110 115 120

Lys Cys Val Leu Pro His Met Ile Glu Arg Lys Gln Gly Lys Ile

125 130 135

Val Thr Val Asn Ser Ile Leu Gly Ile Ile Ser Val Pro Leu Ser

140 145 150

Ile Gly Tyr Cys Ala Ser Lys His Ala Leu Arg Gly Phe Phe Asn

155 160 165

Gly Leu Arg Thr Glu Leu Ala Thr Tyr Pro Gly Ile Ile Val Ser

170 175 180

Asn Ile Cys Pro Gly Pro Val Gln Ser Asn Ile Val Glu Asn Ser

185 190 195



Leu Ala Gly Glu Val Thr Lys Thr Ile Gly Asn Asn Gly Asp Gln  
200 205 210

Ser His Lys Met Thr Thr Ser Arg Cys Val Arg Leu Met Leu Ile  
215 220 225

Ser Met Ala Asn Asp Leu Lys Glu Val Trp Ile Ser Glu Gln Pro  
230 235 240

Phe Leu Leu Val Thr Tyr Leu Trp Gln Tyr Met Pro Thr Trp Ala  
245 250 255

Trp Trp Ile Thr Asn Lys Met Gly Lys Lys Arg Ile Glu Asn Phe  
260 265 270

Lys Ser Gly Val Asp Ala Asp Ser Ser Tyr Phe Lys Ile Phe Lys  
275 280 285

Thr Lys His Asp

<210> 125

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 125

gcaatgaact gggagctgc 19

<210> 126

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 126

ctgtgaatag catcctggg 19

<210> 127

<211> 20

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 127  
ctttcaagc cactggaggg 20

<210> 128  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 128  
ctgtagacat ccaagctggt atcc 24

<210> 129  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 129  
aagagtctgc atccacacca ctc 23

<210> 130  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 130  
acctgacgt actatgggcc gaggggcagg gacgacgcc agaag 46

<210> 131  
<211> 2365  
<212> DNA

<213> Homo sapiens

<400> 131

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tgttacaaaa taaaa 2365

<210> 132

<211> 571

<212> PRT

<213> Homo sapiens

<400> 132

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20 25 30

Ile Thr Thr Tyr Ala Ile Asn Val Ser Leu Met Trp Leu Ser Phe

35 40 45

Arg Lys Val Gln Glu Pro Gln Gly Lys Ala Lys Arg His Gly Asn

50 55 60

Thr Val Pro Gly Glu Trp Pro Trp Gln Ala Ser Val Arg Arg Gln

65 70 75

Gly Ala His Ile Cys Ser Gly Ser Leu Val Ala Asp Thr Trp Val

80 85 90

Leu Thr Ala Ala His Cys Phe Glu Lys Ala Ala Ala Thr Glu Leu

95 100 105

Asn Ser Trp Ser Val Val Leu Gly Ser Leu Gln Arg Glu Gly Leu

110 115 120

Ser Pro Gly Ala Glu Glu Val Gly Val Ala Ala Leu Gln Leu Pro

125 130 135

Arg Ala Tyr Asn His Tyr Ser Gln Gly Ser Asp Leu Ala Leu Leu

140 145 150

Gln Leu Ala His Pro Thr Thr His Thr Pro Leu Cys Leu Pro Gln

155	160	165
Pro Ala His Arg Phe Pro Phe Gly Ala Ser Cys Trp Ala Thr Gly		
170	175	180
Trp Asp Gln Asp Thr Ser Asp Ala Pro Gly Thr Leu Arg Asn Leu		
185	190	195
Arg Leu Arg Leu Ile Ser Arg Pro Thr Cys Asn Cys Ile Tyr Asn		
200	205	210
Gln Leu His Gln Arg His Leu Ser Asn Pro Ala Arg Pro Gly Met		
215	220	225
Leu Cys Gly Gly Pro Gln Pro Gly Val Gln Gly Pro Cys Gln Gly		
230	235	240
Asp Ser Gly Gly Pro Val Leu Cys Leu Glu Pro Asp Gly His Trp		
245	250	255
Val Gln Ala Gly Ile Ile Ser Phe Ala Ser Ser Cys Ala Gln Glu		
260	265	270
Asp Ala Pro Val Leu Leu Thr Asn Thr Ala Ala His Ser Ser Trp		
275	280	285
Leu Gln Ala Arg Val Gln Gly Ala Ala Phe Leu Ala Gln Ser Pro		
290	295	300
Glu Thr Pro Glu Met Ser Asp Glu Asp Ser Cys Val Ala Cys Gly		
305	310	315
Ser Leu Arg Thr Ala Gly Pro Gln Ala Gly Ala Pro Ser Pro Trp		
320	325	330
Pro Trp Glu Ala Arg Leu Met His Gln Gly Gln Leu Ala Cys Gly		
335	340	345
Gly Ala Leu Val Ser Glu Glu Ala Val Leu Thr Ala Ala His Cys		
350	355	360
Phe Ile Gly Arg Gln Ala Pro Glu Glu Trp Ser Val Gly Leu Gly		
365	370	375
Thr Arg Pro Glu Glu Trp Gly Leu Lys Gln Leu Ile Leu His Gly		

380	385	390
Ala Tyr Thr His Pro Glu Gly Gly Tyr Asp Met Ala Leu Leu Leu		
395	400	405
Leu Ala Gln Pro Val Thr Leu Gly Ala Ser Leu Arg Pro Leu Cys		
410	415	420
Leu Pro Tyr Pro Asp His His Leu Pro Asp Gly Glu Arg Gly Trp		
425	430	435
Val Leu Gly Arg Ala Arg Pro Gly Ala Gly Ile Ser Ser Leu Gln		
440	445	450
Thr Val Pro Val Thr Leu Leu Gly Pro Arg Ala Cys Ser Arg Leu		
455	460	465
His Ala Ala Pro Gly Gly Asp Gly Ser Pro Ile Leu Pro Gly Met		
470	475	480
Val Cys Thr Ser Ala Val Gly Glu Leu Pro Ser Cys Glu Gly Leu		
485	490	495
Ser Gly Ala Pro Leu Val His Glu Val Arg Gly Thr Trp Phe Leu		
500	505	510
Ala Gly Leu His Ser Phe Gly Asp Ala Cys Gln Gly Pro Ala Arg		
515	520	525
Pro Ala Val Phe Thr Ala Leu Pro Ala Tyr Glu Asp Trp Val Ser		
530	535	540
Ser Leu Asp Trp Gln Val Tyr Phe Ala Glu Glu Pro Glu Pro Glu		
545	550	555
Ala Glu Pro Gly Ser Cys Leu Ala Asn Ile Ser Gln Pro Thr Ser		
560	565	570

Cys

<210> 133

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 133

cctgtgctgt gcctcgagcc tgac 24

<210> 134

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 134

gtgggcagca gtagcaccg cctc 24

<210> 135

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 135

ggctggcatc atcagctttg catcaagctg tgcccaggag gacgc 45

<210> 136

<211> 1998

<212> DNA

<213> Homo sapiens

<400> 136

cgggccgccc ccggccccc ttcgggccgg gcctcgctgc ggcggcgact 50

gagccaggct gggccgcgtc cctgagtcct agagtcggcg cggcgcggca 100

ggggcagcct tccaccacgg ggagcccagc tgcagccgc ctacaggaa 150

gatgtgcgt cggcggggca gccctggcat ggggtgcat gtgggtgcag 200

ccctgggagc actgtggttc tgcctcacag gagccctgga ggtccagtc 250

cctgaagacc cagtgtggc actggtggc accgatgcca ccctgtgtg 300



ctccttctcc cctgagcctg gcttcagcct ggcacagctc aacctcatct 350  
ggcagctgac agatacaaaa cagctgggtgc acagctttgc tgagggccag 400  
gaccagggga gcgcctatgc caaccgcacg gccctcttcc cggacctgct 450  
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ctctgacagg tgggtcctt ctcaaagga tgcgatacac agaccactgt 1250  
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 tccaatggcc gtgatacact agtgaatcatg ttcagccctg cttccacctg 1600  
 catagaatct ttttcttca gacagggaca gtgcggcctc aacatctcct 1650  
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 atgccttccg gatgtcatct ctccctgccc caggaatgga agatgtgagg 1900  
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 atttgggga aaataaatgt cttgtaaaa aaaaaaaaaa aaaaaaaaa 1998

<210> 137  
 <211> 316  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 233  
 <223> unknown amino acid

<400> 137  
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 Ala Ala Leu Gly Ala Leu Trp Phe Cys Leu Thr Gly Ala Leu Glu  
 20 25 30  
 Val Gln Val Pro Glu Asp Pro Val Val Ala Leu Val Gly Thr Asp  
 35 40 45  
 Ala Thr Leu Cys Cys Ser Phe Ser Pro Glu Pro Gly Phe Ser Leu  
 50 55 60

Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu  
65 70 75

Val His Ser Phe Ala Glu Gly Gln Asp Gln Gly Ser Ala Tyr Ala  
80 85 90

Asn Arg Thr Ala Leu Phe Pro Asp Leu Leu Ala Gln Gly Asn Ala  
95 100 105

Ser Leu Arg Leu Gln Arg Val Arg Val Ala Asp Glu Gly Ser Phe  
110 115 120

Thr Cys Phe Val Ser Ile Arg Asp Phe Gly Ser Ala Ala Val Ser  
125 130 135

Leu Gln Val Ala Ala Pro Tyr Ser Lys Pro Ser Met Thr Leu Glu  
140 145 150

Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr Val Thr Ile Thr Cys  
155 160 165

Ser Ser Tyr Gln Gly Tyr Pro Glu Ala Glu Val Phe Trp Gln Asp  
170 175 180

Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr Thr Ser Gln Met  
185 190 195

Ala Asn Glu Gln Gly Leu Phe Asp Val His Ser Val Leu Arg Val  
200 205 210

Val Leu Gly Ala Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn Pro  
215 220 225

Val Leu Gln Gln Asp Ala His Xaa Ser Val Thr Ile Thr Gly Gln  
230 235 240

Pro Met Thr Phe Pro Pro Glu Ala Leu Trp Val Thr Val Gly Leu  
245 250 255

Ser Val Cys Leu Ile Ala Leu Leu Val Ala Leu Ala Phe Val Cys  
260 265 270

Trp Arg Lys Ile Lys Gln Ser Cys Glu Glu Glu Asn Ala Gly Ala  
275 280 285

Glu Asp Gln Asp Gly Glu Gly Glu Gly Ser Lys Thr Ala Leu Gln  
290 295 300

Pro Leu Lys His Ser Asp Ser Lys Glu Asp Asp Gly Gln Glu Ile  
305 310 315

Ala

<210> 138

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 138

ctggcacagc tcaacctcat ctgg 24

<210> 139

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 139

gctgtctgtc tgtctcattg 20

<210> 140

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 140

ggacacagta tactgaccac 20

<210> 141

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 141

tgccaaccag gcagctgtaa gtgc 24

<210> 142

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 142

tggaagaaga ggggtggtgat gtgg 24

<210> 143

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 143

cagctgacag acaccaaaca gctggtgcac agtttcaccg aaggc 45

<210> 144

<211> 2336

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 1620, 1673

<223> unknown base

<400> 144

ttcgtgacct ttgagaaaag agttggtggt aaatgtgcca cgtcttctaa 50

gaagggggag tcctgaactt gtctgaagcc cttgtccgta agccttgaac 100

tacgttctta aatctatgaa gtcgaggac ctttcgctgc tttttaggg 150  
acttctttcc ttgcttcagc aacatgaggc ttttctgtg gaacgcggtc 200  
ttgactctgt tcgtcacttc ttgattggg gctttgatcc ctgaaccaga 250  
agtgaaaatt gaagttctcc agaagccatt catctgccat cgcaagacca 300  
aaggagggga ttgatgttg gtccactatg aaggctactt agaaaaggac 350  
ggctccttat ttcactccac tcacaaacat aacaatggc agcccatttg 400  
gtttaccctg ggcatcctgg aggctctcaa aggttgggac cagggttga 450  
aaggaatgtg tgtaggagag aagagaaagc tcattcattcc tctgtcttg 500  
ggctatggaa aagaaggaaa aggtaaaatt cccccagaaa gtacactgat 550  
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gagttataga gatacatcta ccctttta atagcactca tcttcaaga 850  
gagggcagtc atctttaag aacattttat tttatacaa tgttcttct 900  
tgctttgttt tttatttta tatattttt ctgactccta tttaagaac 950  
cccttaggtt tctaagtacc catttcttc tgataagttt ttgggaagaa 1000  
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caactgggaa tataccagca catgagacca ggtagatga caaattagca 1150  
ccctatattt ctgcttcct ctatttctc caagtagag gtcaacattt 1200  
gaaaagcctt ttgcaatagc ccaaggcttg ctatttcat gttataatga 1250

aatagtttat gtgtaactgg cictgagtct ctgcttgagg accagaggaa 1300  
aatggttggt ggacctgact tgtaatggc tactgcttta ctaaggagat 1350  
gtgcaatgct gaagttagaa acaagggttaa tagccaggca tggaggctca 1400  
tgcctgtaat cccagcactt tgggaggctg aggcggggcg atcacctgag 1450  
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taaaaataca aagtagcccg gcgtgggtgat gcgtgcctgt aatcccagct 1550  
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cggtaagccg agatcacctn cagcctggac actctgtctc gaaaaaagaa 1650  
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taggacttaa gctgatgaag cttggctcct agtgattggt ggcctattat 1750  
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agtatattat actacaataa cattgtatca taagataaag tagtaaacca 1950  
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tcacttgaga tcaggagttc aagaccagcc tggccaacat ggtgaaacct 2100  
tgtctctact aaaaatacaa aaattagcca ggcgtgggtg tgcacacctg 2150  
tagtcccagc tactcgggag gctgagacag gagatttgct tgaacccggg 2200  
aggcggaggt tgcagtgagc caagattgtg ccactgcact ccagcctggg 2250  
tgacagagca agactccatc tcaaaaaaaaa aaaaaagaag cagacctaca 2300  
gcagctacta ttgaataaat acctatcctg gatttt 2336

<211> 211

<212> PRT

<213> Homo sapiens

<400> 145

Met Arg Leu Phe Leu Trp Asn Ala Val Leu Thr Leu Phe Val Thr  
1 5 10 15

Ser Leu Ile Gly Ala Leu Ile Pro Glu Pro Glu Val Lys Ile Glu  
20 25 30

Val Leu Gln Lys Pro Phe Ile Cys His Arg Lys Thr Lys Gly Gly  
35 40 45

Asp Leu Met Leu Val His Tyr Glu Gly Tyr Leu Glu Lys Asp Gly  
50 55 60

Ser Leu Phe His Ser Thr His Lys His Asn Asn Gly Gln Pro Ile  
65 70 75

Trp Phe Thr Leu Gly Ile Leu Glu Ala Leu Lys Gly Trp Asp Gln  
80 85 90

Gly Leu Lys Gly Met Cys Val Gly Glu Lys Arg Lys Leu Ile Ile  
95 100 105

Pro Pro Ala Leu Gly Tyr Gly Lys Glu Gly Lys Gly Lys Ile Pro  
110 115 120

Pro Glu Ser Thr Leu Ile Phe Asn Ile Asp Leu Leu Glu Ile Arg  
125 130 135

Asn Gly Pro Arg Ser His Glu Ser Phe Gln Glu Met Asp Leu Asn  
140 145 150

Asp Asp Trp Lys Leu Ser Lys Asp Glu Val Lys Ala Tyr Leu Lys  
155 160 165

Lys Glu Phe Glu Lys His Gly Ala Val Val Asn Glu Ser His His  
170 175 180

Asp Ala Leu Val Glu Asp Ile Phe Asp Lys Glu Asp Glu Asp Lys  
185 190 195

Asp Gly Phe Ile Ser Ala Arg Glu Phe Thr Tyr Lys His Asp Glu



200

205

210

Leu

<210> 146

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 146

ctttccttgc ttcagcaaca tgaggc 26

<210> 147

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 147

gcccagagca ggaggaatga tgagc 25

<210> 148

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 148

gtggaacgcg gtcttgactc tgttcgtcac ttctttgatt ggggctttg 49

<210> 149

<211> 2196

<212> DNA

<213> Homo sapiens

<400> 149

aataaagctt ccttaatgtt gtatatgtct ttgaagtaca tccgtgcatt 50

tttttttagc atccaacat tcttcccttg tagttctgc cccctcaa 100  
caccctctcc cgtagccac ccgactaaca tctcagtctc tgaaaatgca 150  
cagagatgcc tggtacctc gccctgcctt cagcctcacg gggctcagtc 200  
tctttttctc ttgttgcca ccaggacgga gcatggaggt cacagtacct 250  
gccaccctca acgtctcaa tggctctgac gcccgcctgc cctgcacctt 300  
caactcctgc tacacagtga accacaaaca gtttccctg aactggactt 350  
accaggagtg caacaactgc tctgaggaga tgttctcca gtccgcatg 400  
aagatcatta acctgaagct ggagcgggtt caagaccgcg tggagtctc 450  
agggaaaccc agcaagtacg atgtgtcggg gatgctgaga aacgtgcagc 500  
cggaggatga ggggatttac aactgctaca tcatgaaccc ccctgaccgc 550  
caccgtggcc atggcaagat ccactgcag gtcctcatgg aagagcccc 600  
tgagcgggac tccacgggtg ccgtgattgt gggcgcctcc gtcgggggct 650  
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caagacggac ggtgaaggca acccgatga tggcgccaag tagtggttg 800  
ccggccctgc agcctccctg gtccctctc ctccctctc cgcctgtac 850  
agtgacctg cctgtctgct ctgtgtgtc ttccctgac ctaggaccc 900  
agggcccacc tgggcctcc tgaaccccg acttctatc tcccacctg 950  
caccaagagt gaccactct ctccatccg agaaacctgc catgctctg 1000  
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tgcggccacg ctactcgctc ctctcccaac aactcccttc gtggggacaa 1900  
aagtgacaat ttaggccag gcacagtggc tcacgcctgt aatcccagca 1950  
ctttgggagg ccaaggcggg tggattacct ccatctgttt agtagaatg 2000  
ggcaaaacc catcttact aaaaatacaa gaattagctg ggcgtggtgg 2050  
cgtgtgcctg taatcccagc tatttgggag gctgaggcag gagaatcgct 2100  
tgagcccggg aagcagaggt tgacgtgaac tgagatagt atagtccac 2150  
tgcaattcag cctgggtgac atagagagac tccatctcaa aaaaaa 2196

<210> 150

<211> 215

<212> PRT

<213> Homo sapiens

<400> 150

Met His Arg Asp Ala Trp Leu Pro Arg Pro Ala Phe Ser Leu Thr  
1 5 10 15

Gly Leu Ser Leu Phe Phe Ser Leu Val Pro Pro Gly Arg Ser Met  
20 25 30

Glu Val Thr Val Pro Ala Thr Leu Asn Val Leu Asn Gly Ser Asp  
35 40 45

Ala Arg Leu Pro Cys Thr Phe Asn Ser Cys Tyr Thr Val Asn His  
50 55 60

Lys Gln Phe Ser Leu Asn Trp Thr Tyr Gln Glu Cys Asn Asn Cys  
65 70 75

Ser Glu Glu Met Phe Leu Gln Phe Arg Met Lys Ile Ile Asn Leu  
80 85 90

Lys Leu Glu Arg Phe Gln Asp Arg Val Glu Phe Ser Gly Asn Pro  
95 100 105

Ser Lys Tyr Asp Val Ser Val Met Leu Arg Asn Val Gln Pro Glu  
110 115 120

Asp Glu Gly Ile Tyr Asn Cys Tyr Ile Met Asn Pro Pro Asp Arg  
125 130 135

His Arg Gly His Gly Lys Ile His Leu Gln Val Leu Met Glu Glu  
140 145 150

Pro Pro Glu Arg Asp Ser Thr Val Ala Val Ile Val Gly Ala Ser  
155 160 165

Val Gly Gly Phe Leu Ala Val Val Ile Leu Val Leu Met Val Val  
170 175 180

Lys Cys Val Arg Arg Lys Lys Glu Gln Lys Leu Ser Thr Asp Asp  
185 190 195

Leu Lys Thr Glu Glu Glu Gly Lys Thr Asp Gly Glu Gly Asn Pro  
200 205 210

Asp Asp Gly Ala Lys  
215

<210> 151  
<211> 524  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 103, 233  
<223> unknown base

<400> 151  
gttgatatg tctgaagta catccgtgca ttttttttag catccaacca 50  
  
tctcccttg tagttctgc cccctcaaat caccttctcc cttagccac 100  
  
ccnactaaca tctcagtctc tgaaaatgca cagagatgcc tggctacctc 150  
  
gccctgcctt cagcctcaag gggctcagtc tcttttctc ttggtgcca 200  
  
ccaggacgga gcatggaggt ccacagtacc tgnccaccct caacgtcctc 250  
  
aatggctctg acgcccgcct gccctgccct tcaactcctg ctacacagtg 300  
  
aaccacaaac agttctccct gaactggact taccaggagt gcaacaactg 350  
  
ctctgaggag atgttctcc agttccgcat gaagatcatt aacctgaagc 400  
  
tggagcgggt tcaagaccgc gtggagtctc cagggaaccc cagcaagtac 450  
  
gatgtgtcgg tgatgctgag aaacgtgcag ccggaggatg aggggattta 500  
  
caactgctac atcatgaacc cccc 524

<210> 152  
<211> 368  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 56, 123  
<223> unknown base

<400> 152  
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gaggtncaca tacctgccac cctcaacgtc ctcaatggct ttgacgcccg 100  
cctgcctgc accttcaact ccngctacac agtgaaccac aaacagttct 150  
ccctgaactg gatttaccag gagtgcaaca actggctctg aggagatgtt 200  
cctccagttc ccgcatggaa gatcatttaa cctgaaagct ggaagcgggt 250  
ttcaagaacc gcgtggaagt ttctcaggga accccagcaa gtacgatgtg 300  
tcggtgatgc tgagaaacgt gcagccggag gatgagggga ttacaactg 350  
ctacatcatg aaccccc 368

<210> 153  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 153  
acggagcatg gaggtccaca gtac 24

<210> 154  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 154  
gcacgtttct cagcatcacc gac 23

<210> 155  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 155

cgctgcct gcacctcaa ctctgtac acagtgaacc acaaacagtt 50

<210> 156

<211> 2680

<212> DNA

<213> Homo sapiens

<400> 156

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gggtgtctc cgatggcct cctgttctc ttgtgtctgc taatgtgtg 100

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gccttgtggg ctggggctac acacggggtg aggatgtccg aggggctccc 500

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ccgcgagatg atcgaggaga tgtaccagct gtatgggggc cccgtggtgc 600

tggttgcca cagtatgggc aacatgtaca cgtctactt tctgcagcgg 650

cagccgcagg cctggaagga caagtatatc cgggccttcg tgcactggg 700

tgcgccctgg gggggcgtgg ccaagaccct gcgcgtcctg gcttcaggag 750

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cggtcagctg tctccaccag ctggctgtg ccctacaact acacatggtc 850

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atgctgtaaa aaaaaaaaaa aaaaaaaaaa 2680

<210> 157

<211> 412

<212> PRT

<213> Homo Sapien

<400> 157

Met Gly Leu His Leu Arg Pro Tyr Arg Val Gly Leu Leu Pro Asp

1 5 10 15

Gly Leu Leu Phe Leu Leu Leu Leu Met Leu Leu Ala Asp Pro

20 25 30

Ala Leu Pro Ala Gly Arg His Pro Pro Val Val Leu Val Pro Gly

35 40 45

Asp Leu Gly Asn Gln Leu Glu Ala Lys Leu Asp Lys Pro Thr Val

50 55 60

Val His Tyr Leu Cys Ser Lys Lys Thr Glu Ser Tyr Phe Thr Ile

65 70 75

Trp Leu Asn Leu Glu Leu Leu Pro Val Ile Ile Asp Cys Trp  
80 85 90

Ile Asp Asn Ile Arg Leu Val Tyr Asn Lys Thr Ser Arg Ala Thr  
95 100 105

Gln Phe Pro Asp Gly Val Asp Val Arg Val Pro Gly Phe Gly Lys  
110 115 120

Thr Phe Ser Leu Glu Phe Leu Asp Pro Ser Lys Ser Ser Val Gly  
125 130 135

Ser Tyr Phe His Thr Met Val Glu Ser Leu Val Gly Trp Gly Tyr  
140 145 150

Thr Arg Gly Glu Asp Val Arg Gly Ala Pro Tyr Asp Trp Arg Arg  
155 160 165

Ala Pro Asn Glu Asn Gly Pro Tyr Phe Leu Ala Leu Arg Glu Met  
170 175 180

Ile Glu Glu Met Tyr Gln Leu Tyr Gly Gly Pro Val Val Leu Val  
185 190 195

Ala His Ser Met Gly Asn Met Tyr Thr Leu Tyr Phe Leu Gln Arg  
200 205 210

Gln Pro Gln Ala Trp Lys Asp Lys Tyr Ile Arg Ala Phe Val Ser  
215 220 225

Leu Gly Ala Pro Trp Gly Gly Val Ala Lys Thr Leu Arg Val Leu  
230 235 240

Ala Ser Gly Asp Asn Asn Arg Ile Pro Val Ile Gly Pro Leu Lys  
245 250 255

Ile Arg Glu Gln Gln Arg Ser Ala Val Ser Thr Ser Trp Leu Leu  
260 265 270

Pro Tyr Asn Tyr Thr Trp Ser Pro Glu Lys Val Phe Val Gln Thr  
275 280 285

Pro Thr Ile Asn Tyr Thr Leu Arg Asp Tyr Arg Lys Phe Phe Gln  
290 295 300

Asp Ile Gly Phe Glu Asp Gly Trp Leu Met Arg Gln Asp Thr Glu  
305 310 315

Gly Leu Val Glu Ala Thr Met Pro Pro Gly Val Gln Leu His Cys  
320 325 330

Leu Tyr Gly Thr Gly Val Pro Thr Pro Asp Ser Phe Tyr Tyr Glu  
335 340 345

Ser Phe Pro Asp Arg Asp Pro Lys Ile Cys Phe Gly Asp Gly Asp  
350 355 360

Gly Thr Val Asn Leu Lys Ser Ala Leu Gln Cys Gln Ala Trp Gln  
365 370 375

Ser Arg Gln Glu His Gln Val Leu Leu Gln Glu Leu Pro Gly Ser  
380 385 390

Glu His Ile Glu Met Leu Ala Asn Ala Thr Thr Leu Ala Tyr Leu  
395 400 405

Lys Arg Val Leu Leu Gly Pro  
410

<210> 158

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 158

ctggggctac acacggggtg agg 23

<210> 159

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 159

ggtgccgctg cagaaagtag agcg 24

<210> 160  
<211> 45  
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<223> Synthetic oligonucleotide probe

<400> 160  
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<210> 161  
<211> 1512  
<212> DNA  
<213> Homo sapiens

<400> 161  
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gcggcgcttc ctgacgcagc cgcaggtggt ggcgcgcgcc gtgtgcttgg 150  
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<210> 162

<211> 224

<212> PRT

<213> Homo sapiens

<400> 162

Met	Glu	Ser	Gly	Ala	Tyr	Gly	Ala	Ala	Lys	Ala	Gly	Gly	Ser	Phe
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Asp	Leu	Arg	Arg	Phe	Leu	Thr	Gln	Pro	Gln	Val	Val	Ala	Arg	Ala
		20			25			30						

Val Cys Leu Val Phe Ala Leu Ile Val Phe Ser Cys Ile Tyr Gly  
35 40 45

Glu Gly Tyr Ser Asn Ala His Glu Ser Lys Gln Met Tyr Cys Val  
50 55 60

Phe Asn Arg Asn Glu Asp Ala Cys Arg Tyr Gly Ser Ala Ile Gly  
65 70 75

Val Leu Ala Phe Leu Ala Ser Ala Phe Phe Leu Val Val Asp Ala  
80 85 90

Tyr Phe Pro Gln Ile Ser Asn Ala Thr Asp Arg Lys Tyr Leu Val  
95 100 105

Ile Gly Asp Leu Leu Phe Ser Ala Leu Trp Thr Phe Leu Trp Phe  
110 115 120

Val Gly Phe Cys Phe Leu Thr Asn Gln Trp Ala Val Thr Asn Pro  
125 130 135

Lys Asp Val Leu Val Gly Ala Asp Ser Val Arg Ala Ala Ile Thr  
140 145 150

Phe Ser Phe Phe Ser Ile Phe Ser Trp Gly Val Leu Ala Ser Leu  
155 160 165

Ala Tyr Gln Arg Tyr Lys Ala Gly Val Asp Asp Phe Ile Gln Asn  
170 175 180

Tyr Val Asp Pro Thr Pro Asp Pro Asn Thr Ala Tyr Ala Ser Tyr  
185 190 195

Pro Gly Ala Ser Val Asp Asn Tyr Gln Gln Pro Pro Phe Thr Gln  
200 205 210

Asn Ala Glu Thr Thr Glu Gly Tyr Gln Pro Pro Pro Val Tyr  
215 220

<210> 163

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 163

tggtcttcgc cttgatcgtg ttct 24

<210> 164

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 164

gtgtactgag cggcggtag 20

<210> 165

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 165

ctgaaggtga tggctgccct cac 23

<210> 166

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 166

ccaggaggct catgggaaag tcc 23

<210> 167

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 167

ccacgagtct aagcagatgt actgcgtgtt caaccgcaac gaggatgcct 50

<210> 168

<211> 3143

<212> DNA

<213> Homo sapiens

<400> 168

gagccaccta ccctgtccg aggccaggcc tgcagggcct catcggccag 50

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ctggcgggca gggggacgga ggtgatggcg aggaagcgga gccagagggg 150

atgttcaagg cctgtgagga ctccaagaga aaagcccggg gctacctccg 200

cctggtgccc ctgtttgtgc tgctggccct gctcgtgtg gcttcggcgg 250

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caggtgtact caggcagtct gcgtgtactc aatcgccact tctcccagga 350

tcttaccgc cggaatcta gtgccttccg cagtgaacc gccaaagccc 400

agaagatgct caaggagctc atcaccagca cccgcctggg aacttactac 450

aactccagct ccgtctattc ctttggggag ggaccctca cctgettctt 500

ctggttcatt ctccaaatcc ccgagcaccg ccggtgatg ctgagccccg 550

agggtgtgca ggcactgtg gtggaggagc tgctgtccac agtcaacagc 600

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tttgaataa agctgcctga tcaaaaaaaaa aaaaaaaaaa aaa 3143

<211> 802  
<212> PRT  
<213> Homo sapiens

<400> 169

Met Pro Val Ala Glu Ala Pro Gln Val Ala Gly Gly Gln Gly Asp  
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Gly Gly Asp Gly Glu Glu Ala Glu Pro Glu Gly Met Phe Lys Ala  
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Cys Glu Asp Ser Lys Arg Lys Ala Arg Gly Tyr Leu Arg Leu Val  
35 40 45

Pro Leu Phe Val Leu Leu Ala Leu Leu Val Leu Ala Ser Ala Gly  
50 55 60

Val Leu Leu Trp Tyr Phe Leu Gly Tyr Lys Ala Glu Val Met Val  
65 70 75

Ser Gln Val Tyr Ser Gly Ser Leu Arg Val Leu Asn Arg His Phe  
80 85 90

Ser Gln Asp Leu Thr Arg Arg Glu Ser Ser Ala Phe Arg Ser Glu  
95 100 105

Thr Ala Lys Ala Gln Lys Met Leu Lys Glu Leu Ile Thr Ser Thr  
110 115 120

Arg Leu Gly Thr Tyr Tyr Asn Ser Ser Ser Val Tyr Ser Phe Gly  
125 130 135

Glu Gly Pro Leu Thr Cys Phe Phe Trp Phe Ile Leu Gln Ile Pro  
140 145 150

Glu His Arg Arg Leu Met Leu Ser Pro Glu Val Val Gln Ala Leu  
155 160 165

Leu Val Glu Glu Leu Leu Ser Thr Val Asn Ser Ser Ala Ala Val  
170 175 180

Pro Tyr Arg Ala Glu Tyr Glu Val Asp Pro Glu Gly Leu Val Ile  
185 190 195

Leu Glu Ala Ser Val Lys Asp Ile Ala Ala Leu Asn Ser Thr Leu

200	205	210
Gly Cys Tyr Arg Tyr Ser Tyr Val Gly Gln Gly Gln Val Leu Arg		
215	220	225
Leu Lys Gly Pro Asp His Leu Ala Ser Ser Cys Leu Trp His Leu		
230	235	240
Gln Gly Pro Lys Asp Leu Met Leu Lys Leu Arg Leu Glu Trp Thr		
245	250	255
Leu Ala Glu Cys Arg Asp Arg Leu Ala Met Tyr Asp Val Ala Gly		
260	265	270
Pro Leu Glu Lys Arg Leu Ile Thr Ser Val Tyr Gly Cys Ser Arg		
275	280	285
Gln Glu Pro Val Val Glu Val Leu Ala Ser Gly Ala Ile Met Ala		
290	295	300
Val Val Trp Lys Lys Gly Leu His Ser Tyr Tyr Asp Pro Phe Val		
305	310	315
Leu Ser Val Gln Pro Val Val Phe Gln Ala Cys Glu Val Asn Leu		
320	325	330
Thr Leu Asp Asn Arg Leu Asp Ser Gln Gly Val Leu Ser Thr Pro		
335	340	345
Tyr Phe Pro Ser Tyr Tyr Ser Pro Gln Thr His Cys Ser Trp His		
350	355	360
Leu Thr Val Pro Ser Leu Asp Tyr Gly Leu Ala Leu Trp Phe Asp		
365	370	375
Ala Tyr Ala Leu Arg Arg Gln Lys Tyr Asp Leu Pro Cys Thr Gln		
380	385	390
Gly Gln Trp Thr Ile Gln Asn Arg Arg Leu Cys Gly Leu Arg Ile		
395	400	405
Leu Gln Pro Tyr Ala Glu Arg Ile Pro Val Val Ala Thr Ala Gly		
410	415	420
Ile Thr Ile Asn Phe Thr Ser Gln Ile Ser Leu Thr Gly Pro Gly		

425	430	435
Val Arg Val His Tyr Gly Leu Tyr Asn Gln Ser Asp Pro Cys Pro		
440	445	450
Gly Glu Phe Leu Cys Ser Val Asn Gly Leu Cys Val Pro Ala Cys		
455	460	465
Asp Gly Val Lys Asp Cys Pro Asn Gly Leu Asp Glu Arg Asn Cys		
470	475	480
Val Cys Arg Ala Thr Phe Gln Cys Lys Glu Asp Ser Thr Cys Ile		
485	490	495
Ser Leu Pro Lys Val Cys Asp Gly Gln Pro Asp Cys Leu Asn Gly		
500	505	510
Ser Asp Glu Glu Gln Cys Gln Glu Gly Val Pro Cys Gly Thr Phe		
515	520	525
Thr Phe Gln Cys Glu Asp Arg Ser Cys Val Lys Lys Pro Asn Pro		
530	535	540
Gln Cys Asp Gly Arg Pro Asp Cys Arg Asp Gly Ser Asp Glu Glu		
545	550	555
His Cys Asp Cys Gly Leu Gln Gly Pro Ser Ser Arg Ile Val Gly		
560	565	570
Gly Ala Val Ser Ser Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu		
575	580	585
Gln Val Arg Gly Arg His Ile Cys Gly Gly Ala Leu Ile Ala Asp		
590	595	600
Arg Trp Val Ile Thr Ala Ala His Cys Phe Gln Glu Asp Ser Met		
605	610	615
Ala Ser Thr Val Leu Trp Thr Val Phe Leu Gly Lys Val Trp Gln		
620	625	630
Asn Ser Arg Trp Pro Gly Glu Val Ser Phe Lys Val Ser Arg Leu		
635	640	645
Leu Leu His Pro Tyr His Glu Glu Asp Ser His Asp Tyr Asp Val		

650	655	660
Ala Leu Leu Gln Leu Asp His Pro Val Val Arg Ser Ala Ala Val		
665	670	675
Arg Pro Val Cys Leu Pro Ala Arg Ser His Phe Phe Glu Pro Gly		
680	685	690
Leu His Cys Trp Ile Thr Gly Trp Gly Ala Leu Arg Glu Gly Gly		
695	700	705
Pro Ile Ser Asn Ala Leu Gln Lys Val Asp Val Gln Leu Ile Pro		
710	715	720
Gln Asp Leu Cys Ser Glu Ala Tyr Arg Tyr Gln Val Thr Pro Arg		
725	730	735
Met Leu Cys Ala Gly Tyr Arg Lys Gly Lys Lys Asp Ala Cys Gln		
740	745	750
Gly Asp Ser Gly Gly Pro Leu Val Cys Lys Ala Leu Ser Gly Arg		
755	760	765
Trp Phe Leu Ala Gly Leu Val Ser Trp Gly Leu Gly Cys Gly Arg		
770	775	780
Pro Asn Tyr Phe Gly Val Tyr Thr Arg Ile Thr Gly Val Ile Ser		
785	790	795
Trp Ile Gln Gln Val Val Thr		
800		

<210> 170

<211> 1327

<212> DNA

<213> Homo sapiens

<400> 170

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tgactatgg cttgtacaac cagtcggacc cctgccctgg agagttcctc 200

tgttctgtga atggactctg tgtccctgcc tgtgatgggg tcaaggactg 250  
ccccaacggc ctggatgaga gaaactgcgt ttgcagagcc acattccagt 300  
gcaaagagga cagcacatgc atctcactgc ccaaggcttg tgatgggcag 350  
cctgattgtc tcaacggcag cgatgaagag cagtgccagg aaggggtgcc 400  
atgtgggaca ttcaccttcc agtgtgagga cggagctgc gtgaagaagc 450  
ccaacccgca gtgtgatggg cggcccgact gcagggacgg ctcggatgag 500  
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agctgtgtcc tccgaggggtg agtggccatg gcaggccagc ctccaggttc 600  
ggggctcgaca catctgtggg gggggccctca tcgtgaccg ctgggtgata 650  
acagctgccc actgcttcca ggaggacagc atggcctcca cgggtgctgtg 700  
gaccgtgttc ctgggcaagg tgtggcagaa ctgcgctgg cctggagagg 750  
tgtccttcaa ggtgagccgc ctgctcctgc acccgtacca cgaagaggac 800  
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ctcgccgccc gtgcgccccg tctgcctgcc cgcgcgtcc cacttcttcg 900  
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cccgcacac aggtgtgatc agctggatcc agcaagtgtg gacctgagga 1250  
actgcccc tgcaaagcag ggcccacctc ctggactcag agagcccagg 1300  
gcaactgcca agcaggggga caagtat 1327

<210> 171  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 171  
taacagctgc ccactgcttc cagg 24

<210> 172  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 172  
taatccagca gtgcaggccg gg 22

<210> 173  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 173  
atggcctcca cggctgtgtg gaccgtgttc ctgggcaagg tgtggcagaa 50

<210> 174  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 174  
tgcctatgca ctgaggaggc agaag 25

<210> 175



<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 175  
aggcagggac acagagtcca ttcac 25

<210> 176  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 176  
agtatgattt gccgtgcacc cagggccagt ggacgatcca gaacaggagg 50

<210> 177  
<211> 1510  
<212> DNA  
<213> Homo sapiens

<400> 177  
ggacgagggc agatctcgtt ctggggcaag ccgttgacac tcgctccctg 50  
ccaccgcccc ggctccgtgc cgccaagttt tcattttcca cttctctgc 100  
ctccagtecc ccagccccctg gccgagagaa gggctctacc ggccgggatt 150  
gctggaaaca ccaagagggtg gttttgttt tttaaaactt ctgtttcttg 200  
ggaggggggtg tggcgggggca ggatgagcaa ctccgttcct ctgctctgtt 250  
tctggagcct ctgctattgc ttgctgcgg ggagccccgt accttttggt 300  
ccagagggac ggctggaaga taagctccac aaacccaaag ctacacagac 350  
tgagggtcaaa ccatctgtga ggtttaacct ccgcacctcc aaggaccag 400  
agcatgaagg atgctacctc tccgtcggcc acagccagcc cttagaagac 450

tgcagtttca acatgacagc taaaaccttt ttcatcattc acggatggac 500  
gatgagcggg atctttgaaa actggctgca caaactcgtg tcagccctgc 550  
acacaagaga gaaagacgcc aatgtagtgtg tgggtgactg gctccccctg 600  
gcccaccagc ttacacgga tgcgggtcaat aataccagggtg tgggtgggaca 650  
cagcattgcc aggatgctcg actggctgca ggagaaggac gattttctc 700  
tcgggaatgt ccacttgatc ggctacagcc tcggagcgcg cgtggccggg 750  
tatgcaggca acttcgtgaa aggaacgggtg ggccgaatca caggtttga 800  
tcctgccggg cccatgtttg aaggggccga catccacaag aggtctctc 850  
cggacgatgc agattttgtg gatgtcctcc acacctacac gcgttcctc 900  
ggcttgagca ttgtattca gatgcctgtg ggccacattg acatctacc 950  
caatgggggt gacttcagc caggctgtgg actcaacgat gtcttggat 1000  
caattgcata tggaacaatc acagaggtgg taaaatgtga gcatgagcga 1050  
gccgtccacc tctttgtga ctctctgtg aatcaggaca agccgagttt 1100  
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aataaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500  
aaaaaaaaaa 1510

<211> 354  
<212> PRT  
<213> Homo sapiens

<400> 178

Met Ser Asn Ser Val Pro Leu Leu Cys Phe Trp Ser Leu Cys Tyr  
1 5 10 15

Cys Phe Ala Ala Gly Ser Pro Val Pro Phe Gly Pro Glu Gly Arg  
20 25 30

Leu Glu Asp Lys Leu His Lys Pro Lys Ala Thr Gln Thr Glu Val  
35 40 45

Lys Pro Ser Val Arg Phe Asn Leu Arg Thr Ser Lys Asp Pro Glu  
50 55 60

His Glu Gly Cys Tyr Leu Ser Val Gly His Ser Gln Pro Leu Glu  
65 70 75

Asp Cys Ser Phe Asn Met Thr Ala Lys Thr Phe Phe Ile Ile His  
80 85 90

Gly Trp Thr Met Ser Gly Ile Phe Glu Asn Trp Leu His Lys Leu  
95 100 105

Val Ser Ala Leu His Thr Arg Glu Lys Asp Ala Asn Val Val Val  
110 115 120

Val Asp Trp Leu Pro Leu Ala His Gln Leu Tyr Thr Asp Ala Val  
125 130 135

Asn Asn Thr Arg Val Val Gly His Ser Ile Ala Arg Met Leu Asp  
140 145 150

Trp Leu Gln Glu Lys Asp Asp Phe Ser Leu Gly Asn Val His Leu  
155 160 165

Ile Gly Tyr Ser Leu Gly Ala His Val Ala Gly Tyr Ala Gly Asn  
170 175 180

Phe Val Lys Gly Thr Val Gly Arg Ile Thr Gly Leu Asp Pro Ala  
185 190 195

Gly Pro Met Phe Glu Gly Ala Asp Ile His Lys Arg Leu Ser Pro

200	205	210
Asp Asp Ala Asp Phe Val Asp Val Leu His Thr Tyr Thr Arg Ser		
215	220	225
Phe Gly Leu Ser Ile Gly Ile Gln Met Pro Val Gly His Ile Asp		
230	235	240
Ile Tyr Pro Asn Gly Gly Asp Phe Gln Pro Gly Cys Gly Leu Asn		
245	250	255
Asp Val Leu Gly Ser Ile Ala Tyr Gly Thr Ile Thr Glu Val Val		
260	265	270
Lys Cys Glu His Glu Arg Ala Val His Leu Phe Val Asp Ser Leu		
275	280	285
Val Asn Gln Asp Lys Pro Ser Phe Ala Phe Gln Cys Thr Asp Ser		
290	295	300
Asn Arg Phe Lys Lys Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg		
305	310	315
Cys Asn Ser Ile Gly Tyr Asn Ala Lys Lys Met Arg Asn Lys Arg		
320	325	330
Asn Ser Lys Met Tyr Leu Lys Thr Arg Ala Gly Met Pro Phe Arg		
335	340	345
Gly Asn Leu Gln Ser Leu Glu Cys Pro		
350		

<210> 179

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 179

gtgagcatga gcgagccgtc cac 23

<210> 180

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 180

gctattacaa cggttcttgc ggcagc 26

<210> 181

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 181

ttgactctct ggtgaatcag gacaagccga gttttgcctt ccag 44

<210> 182

<211> 3240

<212> DNA

<213> Homo sapiens

<400> 182

cggacgcgtg ggcggacgcg tgggcctggg caagggccgg ggcgccgggc 50

cgagccacct ctccccctcc cccgcttccc tgtcgcgctc cgctggctgg 100

acgcgctgga ggagtggagc agcacccggc cggccctggg ggctgacagt 150

cggcaaagtt tggcccgaag aggaagtgtt ctcaaaccgc ggcaggtggc 200

gaccaggcca gaccaggggc gctcgtgcc tgcgggcggg ctgtaggcga 250

gggcgcgccc cagtgccgag acccggggct tcaggagccg gccccgggag 300

agaagagtgc ggcggcggac ggagaaaaca actccaaagt tggcgaaagg 350

caccgcccct actccggggc tgccgccgcc tccccgccc cagccctggc 400

atccagagta cgggtcagc ccgggcatg gagccccct ggggaggcgg 450

caccagggag cctgggcgcc cggggctccg ccgcgacccc atcgggtaga 500

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gttctgcccc gcaaggtcat tacagctgca gtcattggca gcctagtgtg 1900  
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 ctcacaaaaa gagtgcaca aatgcttcta ttccatagct acggcattgc 3200  
 tcagtaagtt gaggtcaaaa ataaaggaat catacatctc 3240

<210> 183

<211> 713

<212> PRT

<213> Homo sapiens

<400> 183

Met Leu Leu Ala Thr Leu Leu Leu Leu Leu Gly Gly Ala Leu

1 5 10 15

Ala His Pro Asp Arg Ile Ile Phe Pro Asn His Ala Cys Glu Asp

20 25 30

Pro Pro Ala Val Leu Leu Glu Val Gln Gly Thr Leu Gln Arg Pro

35 40 45

Leu Val Arg Asp Ser Arg Thr Ser Pro Ala Asn Cys Thr Trp Leu

50 55 60

Ile Leu Gly Ser Lys Glu Gln Thr Val Thr Ile Arg Phe Gln Lys

65 70 75

Leu His Leu Ala Cys Gly Ser Glu Arg Leu Thr Leu Arg Ser Pro

80 85 90

Leu Gln Pro Leu Ile Ser Leu Cys Glu Ala Pro Pro Ser Pro Leu

95 100 105



Gln Leu Pro Gly Gly Asn Val Thr Ile Thr Tyr Ser Tyr Ala Gly  
110 115 120

Ala Arg Ala Pro Met Gly Gln Gly Phe Leu Leu Ser Tyr Ser Gln  
125 130 135

Asp Trp Leu Met Cys Leu Gln Glu Glu Phe Gln Cys Leu Asn His  
140 145 150

Arg Cys Val Ser Ala Val Gln Arg Cys Asp Gly Val Asp Ala Cys  
155 160 165

Gly Asp Gly Ser Asp Glu Ala Gly Cys Ser Ser Asp Pro Phe Pro  
170 175 180

Gly Leu Thr Pro Arg Pro Val Pro Ser Leu Pro Cys Asn Val Thr  
185 190 195

Leu Glu Asp Phe Tyr Gly Val Phe Ser Ser Pro Gly Tyr Thr His  
200 205 210

Leu Ala Ser Val Ser His Pro Gln Ser Cys His Trp Leu Leu Asp  
215 220 225

Pro His Asp Gly Arg Arg Leu Ala Val Arg Phe Thr Ala Leu Asp  
230 235 240

Leu Gly Phe Gly Asp Ala Val His Val Tyr Asp Gly Pro Gly Pro  
245 250 255

Pro Glu Ser Ser Arg Leu Leu Arg Ser Leu Thr His Phe Ser Asn  
260 265 270

Gly Lys Ala Val Thr Val Glu Thr Leu Ser Gly Gln Ala Val Val  
275 280 285

Ser Tyr His Thr Val Ala Trp Ser Asn Gly Arg Gly Phe Asn Ala  
290 295 300

Thr Tyr His Val Arg Gly Tyr Cys Leu Pro Trp Asp Arg Pro Cys  
305 310 315

Gly Leu Gly Ser Gly Leu Gly Ala Gly Glu Gly Leu Gly Glu Arg  
320 325 330

Cys Tyr Ser Glu Ala Gln Arg Cys Asp Gly Ser Trp Asp Cys Ala  
335 340 345

Asp Gly Thr Asp Glu Glu Asp Cys Pro Gly Cys Pro Pro Gly His  
350 355 360

Phe Pro Cys Gly Ala Ala Gly Thr Ser Gly Ala Thr Ala Cys Tyr  
365 370 375

Leu Pro Ala Asp Arg Cys Asn Tyr Gln Thr Phe Cys Ala Asp Gly  
380 385 390

Ala Asp Glu Arg Arg Cys Arg His Cys Gln Pro Gly Asn Phe Arg  
395 400 405

Cys Arg Asp Glu Lys Cys Val Tyr Glu Thr Trp Val Cys Asp Gly  
410 415 420

Gln Pro Asp Cys Ala Asp Gly Ser Asp Glu Trp Asp Cys Ser Tyr  
425 430 435

Val Leu Pro Arg Lys Val Ile Thr Ala Ala Val Ile Gly Ser Leu  
440 445 450

Val Cys Gly Leu Leu Leu Val Ile Ala Leu Gly Cys Thr Cys Lys  
455 460 465

Leu Tyr Ala Ile Arg Thr Gln Glu Tyr Ser Ile Phe Ala Pro Leu  
470 475 480

Ser Arg Met Glu Ala Glu Ile Val Gln Gln Gln Ala Pro Pro Ser  
485 490 495

Tyr Gly Gln Leu Ile Ala Gln Gly Ala Ile Pro Pro Val Glu Asp  
500 505 510

Phe Pro Thr Glu Asn Pro Asn Asp Asn Ser Val Leu Gly Asn Leu  
515 520 525

Arg Ser Leu Leu Gln Ile Leu Arg Gln Asp Met Thr Pro Gly Gly  
530 535 540

Gly Pro Gly Ala Arg Arg Arg Gln Arg Gly Arg Leu Met Arg Arg  
545 550 555

Leu Val Arg Arg Leu Arg Arg Trp Gly Leu Leu Pro Arg Thr Asn  
560 565 570

Thr Pro Ala Arg Ala Ser Glu Ala Arg Ser Gln Val Thr Pro Ser  
575 580 585

Ala Ala Pro Leu Glu Ala Leu Asp Gly Gly Thr Gly Pro Ala Arg  
590 595 600

Glu Gly Gly Ala Val Gly Gly Gln Asp Gly Glu Gln Ala Pro Pro  
605 610 615

Leu Pro Ile Lys Ala Pro Leu Pro Ser Ala Ser Thr Ser Pro Ala  
620 625 630

Pro Thr Thr Val Pro Glu Ala Pro Gly Pro Leu Pro Ser Leu Pro  
635 640 645

Leu Glu Pro Ser Leu Leu Ser Gly Val Val Gln Ala Leu Arg Gly  
650 655 660

Arg Leu Leu Pro Ser Leu Gly Pro Pro Gly Pro Thr Arg Ser Pro  
665 670 675

Pro Gly Pro His Thr Ala Val Leu Ala Leu Glu Asp Glu Asp Asp  
680 685 690

Val Leu Leu Val Pro Leu Ala Glu Pro Gly Val Trp Val Ala Glu  
695 700 705

Ala Glu Asp Glu Pro Leu Leu Thr  
710

<210> 184

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 184

ggctgtcact gtggagacac 20

<210> 185

<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 185  
gcaaggtcat tacagctg 18

<210> 186  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 186  
agaacatagg agcagtccca ctc 23

<210> 187  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 187  
tgctgtgctgc tgcacaatct cag 23

<210> 188  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 188  
ggctattgct tgcctggga cagaccctgt ggcttaggct ctggc 45

<210> 189  
<211> 663

<212> DNA

<213> Homo sapiens

<400> 189

cgagctgggc gagaagtagg ggagggcggt gctccgccgc ggtggcggtt 50

gctatcgctt cgcagaacct actcaggcag ccagctgaga agagttgagg 100

gaaagtgtg ctgtgggtc tgcagacgcg atggataacg tgcagccgaa 150

aataaaacat cgcccccttct gcttcagtgt gaaaggccac gtgaagatgc 200

tgcggctggc actaactgtg acatctatga cctttttat catcgacaa 250

gcccctgaac catatattgt tactactgga ttggaagtca ccgttatctt 300

attttcata cttttatatg tactcagact tgatcgatta atgaagtgtt 350

tattttggcc ttgtctgat attatcaact cactggtaac aacagtattc 400

atgctcatcg tatctgtgtt ggcaactgata ccagaaacca caacattgac 450

agttggtgga ggggtgtttg cacttgtagc agcagtagc tgtcttgccg 500

acggggccct tatttaccgg aagcttctgt tcaatcccag cggtccttac 550

cagaaaaagc ctgtgcatga aaaaaaagaa gttttgtaat ttatattac 600

ttttagttt gatactaagt attaaacata ttctgtatt ctccaaaaa 650

aaaaaaaaa aaa 663

<210> 190

<211> 152

<212> PRT

<213> Homo sapiens

<400> 190

Met Asp Asn Val Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe

1 5 10 15

Ser Val Lys Gly His Val Lys Met Leu Arg Leu Ala Leu Thr Val

20 25 30

Thr Ser Met Thr Phe Phe Ile Ile Ala Gln Ala Pro Glu Pro Tyr

35 40 45

Ile Val Ile Thr Gly Phe Glu Val Thr Val Ile Leu Phe Phe Ile  
50 55 60

Leu Leu Tyr Val Leu Arg Leu Asp Arg Leu Met Lys Trp Leu Phe  
65 70 75

Trp Pro Leu Leu Asp Ile Ile Asn Ser Leu Val Thr Thr Val Phe  
80 85 90

Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu Thr Thr Thr  
95 100 105

Leu Thr Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala Val Cys  
110 115 120

Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe Asn  
125 130 135

Pro Ser Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu  
140 145 150

Val Leu

<210> 191

<211> 495

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 78, 212, 234, 487

<223> unknown base

<400> 191

gggcgagaag taggggaggg cgtgtccgc cgcggtggcg gttgctatcg 50

ttttgcagaa cctactcagg cagccagntg agaagagttg agggaaagtg 100

ctgctgctgg gtctgcagac gcgatggata acgtgcagcc gaaaataaaa 150

catcggccct tctgcttcag tgtgaaaggc cacgtgaaga tgctgcggct 200

ggcactaact gngacatcta tgacctttt tatnatcgca caagcccctg 250

aaccatatat tgttatcact ggatttgaag tcaccgttat cttattttc 300

atactttat atgtactcag acttgatcga ttaatgaagt ggttatttg 350

gcctttgctt gatattatca actcactggt aacaacagta ttcagtctca 400

tcgtatctgt gttggcactg ataccagaaa ccacaacatt gacagttggt 450

ggaggggtgt ttgcactgt gacagcagta tgctgtnttg ccgac 495

<210> 192

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 192

cgttttgcag aacctactca ggcag 25

<210> 193

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 193

cctccaccaa ctgtcaatgt tgtgg 25

<210> 194

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 194

aaagtgtgc tgctgggtct gcagacgca tggataacgt 40

<210> 195  
<211> 1879  
<212> DNA  
<213> Homo sapien

<400> 195  
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cactggcccc ggcgctctg ctgcctctgc tggcccagt gctcctgcgc 150  
gccgccccgg agctggcccc cgcgcccttc acgtgcccc tccgggtggc 200  
cgcgggcacg aaccgcgtag ttgcggccac cccgggaccc gggaccctg 250  
ccgagcgcca cgccgacggc ttggcgctcg ccctggagcc tgcctggcg 300  
tccccgcgg gcgccgcaa ctcttgcc atggtagaca acctgcaggg 350  
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agaagctaca gattctgtt gacactggaa gcagtaact tgccgtggca 450  
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<210> 196

<211> 518

<212> PRT

<213> Homo sapien

<400> 196

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Leu Pro Leu Arg Val Ala Ala Ala Thr Asn Arg Val Val Ala Pro  
35 40 45

Thr Pro Gly Pro Gly Thr Pro Ala Glu Arg His Ala Asp Gly Leu  
50 55 60

Ala Leu Ala Leu Glu Pro Ala Leu Ala Ser Pro Ala Gly Ala Ala  
65 70 75

Asn Phe Leu Ala Met Val Asp Asn Leu Gln Gly Asp Ser Gly Arg  
80 85 90

Gly Tyr Tyr Leu Glu Met Leu Ile Gly Thr Pro Pro Gln Lys Leu  
95 100 105

Gln Ile Leu Val Asp Thr Gly Ser Ser Asn Phe Ala Val Ala Gly  
110 115 120

Thr Pro His Ser Tyr Ile Asp Thr Tyr Phe Asp Thr Glu Arg Ser  
125 130 135

Ser Thr Tyr Arg Ser Lys Gly Phe Asp Val Thr Val Lys Tyr Thr  
140 145 150

Gln Gly Ser Trp Thr Gly Phe Val Gly Glu Asp Leu Val Thr Ile  
155 160 165

Pro Lys Gly Phe Asn Thr Ser Phe Leu Val Asn Ile Ala Thr Ile  
170 175 180

Phe Glu Ser Glu Asn Phe Phe Leu Pro Gly Ile Lys Trp Asn Gly  
185 190 195

Ile Leu Gly Leu Ala Tyr Ala Thr Leu Ala Lys Pro Ser Ser Ser  
200 205 210

Leu Glu Thr Phe Phe Asp Ser Leu Val Thr Gln Ala Asn Ile Pro  
215 220 225

Asn Val Phe Ser Met Gln Met Cys Gly Ala Gly Leu Pro Val Ala  
230 235 240

Gly Ser Gly Thr Asn Gly Gly Ser Leu Val Leu Gly Gly Ile Glu  
245 250 255

Pro Ser Leu Tyr Lys Gly Asp Ile Trp Tyr Thr Pro Ile Lys Glu  
260 265 270

Glu Trp Tyr Tyr Gln Ile Glu Ile Leu Lys Leu Glu Ile Gly Gly  
275 280 285

Gln Ser Leu Asn Leu Asp Cys Arg Glu Tyr Asn Ala Asp Lys Ala  
290 295 300

Ile Val Asp Ser Gly Thr Thr Leu Leu Arg Leu Pro Gln Lys Val  
305 310 315

Phe Asp Ala Val Val Glu Ala Val Ala Arg Ala Ser Leu Ile Pro  
320 325 330

Glu Phe Ser Asp Gly Phe Trp Thr Gly Ser Gln Leu Ala Cys Trp  
335 340 345

Thr Asn Ser Glu Thr Pro Trp Ser Tyr Phe Pro Lys Ile Ser Ile  
350 355 360

Tyr Leu Arg Asp Glu Asn Ser Ser Arg Ser Phe Arg Ile Thr Ile  
365 370 375

Leu Pro Gln Leu Tyr Ile Gln Pro Met Met Gly Ala Gly Leu Asn  
380 385 390

Tyr Glu Cys Tyr Arg Phe Gly Ile Ser Pro Ser Thr Asn Ala Leu  
395 400 405

Val Ile Gly Ala Thr Val Met Glu Gly Phe Tyr Val Ile Phe Asp  
410 415 420

Arg Ala Gln Lys Arg Val Gly Phe Ala Ala Ser Pro Cys Ala Glu  
425 430 435

Ile Ala Gly Ala Ala Val Ser Glu Ile Ser Gly Pro Phe Ser Thr  
440 445 450

Glu Asp Val Ala Ser Asn Cys Val Pro Ala Gln Ser Leu Ser Glu  
455 460 465

Pro Ile Leu Trp Ile Val Ser Tyr Ala Leu Met Ser Val Cys Gly  
470 475 480

Ala Ile Leu Leu Val Leu Ile Val Leu Leu Leu Leu Pro Phe Arg  
485 490 495

Cys Gln Arg Arg Pro Arg Asp Pro Glu Val Val Asn Asp Glu Ser  
500 505 510

Ser Leu Val Arg His Arg Trp Lys  
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<210> 197

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 197

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<210> 198

<211> 19

<212> DNA

<213> Artificial Sequence

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<400> 198

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<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 199

ggatgtagcc agcaactgtg 20

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<223> Synthetic oligonucleotide probe

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gccttggtc gttctctc 19

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<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 201  
ggctctgtgc ctggatgg 18

<210> 202  
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<223> Synthetic oligonucleotide probe

<400> 202  
gacaagacta cctccgttgc tc 22

<210> 203  
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<212> DNA  
<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 203  
tgatgcacag ttcagcacct gttg 24

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<211> 47

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 204

cgctccaagg gctttgacgt cacagtgaag tacacacaag gaagctg 47

<210> 205

<211> 1939

<212> DNA

<213> Homo sapiens

<400> 205

cgctccgcc ttcggaggct gacgcgccg ggcgccgttc caggcctgtg 50

cagggcggat cggcagccgc ctggcggcga tccagggcgg tgcggggcct 100

gggcgggagc cgggaggcgc ggccggcatg gaggcgctgc tgctgggcgc 150

ggggttgctg ctgggcgctt acgtgcttgc ctactacaac ctggtgaagg 200

ccccgccgtg cggcggcatg ggcaacctgc ggggccgcac ggccgtggtc 250

acgggcgcca acagcggcat cggaagatg acggcgctgg agctggcgcg 300

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taaagcgcgt tgaccgcaa aaaaaaaaaa aaaaaaaaaa 1939

<210> 206

<211> 377

<212> PRT

<213> Homo sapiens

<400> 206

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Val Leu Val Tyr Tyr Asn Leu Val Lys Ala Pro Pro Cys Gly Gly  
20 25 30

Met Gly Asn Leu Arg Gly Arg Thr Ala Val Val Thr Gly Ala Asn  
35 40 45

Ser Gly Ile Gly Lys Met Thr Ala Leu Glu Leu Ala Arg Arg Gly  
50 55 60

Ala Arg Val Val Leu Ala Cys Arg Ser Gln Glu Arg Gly Glu Ala  
65 70 75

Ala Ala Phe Asp Leu Arg Gln Glu Ser Gly Asn Asn Glu Val Ile  
80 85 90

Phe Met Ala Leu Asp Leu Ala Ser Leu Ala Ser Val Arg Ala Phe  
95 100 105

Ala Thr Ala Phe Leu Ser Ser Glu Pro Arg Leu Asp Ile Leu Ile  
110 115 120

His Asn Ala Gly Ile Ser Ser Cys Gly Arg Thr Arg Glu Ala Phe  
125 130 135

Asn Leu Leu Leu Arg Val Asn His Ile Gly Pro Phe Leu Leu Thr  
140 145 150

His Leu Leu Leu Pro Cys Leu Lys Ala Cys Ala Pro Ser Arg Val  
155 160 165

Val Val Val Ala Ser Ala Ala His Cys Arg Gly Arg Leu Asp Phe  
170 175 180

Lys Arg Leu Asp Arg Pro Val Val Gly Trp Arg Gln Glu Leu Arg



185	190	195
Ala Tyr Ala Asp Thr Lys Leu Ala Asn Val Leu Phe Ala Arg Glu		
200	205	210
Leu Ala Asn Gln Leu Glu Ala Thr Gly Val Thr Cys Tyr Ala Ala		
215	220	225
His Pro Gly Pro Val Asn Ser Glu Leu Phe Leu Arg His Val Pro		
230	235	240
Gly Trp Leu Arg Pro Leu Leu Arg Pro Leu Ala Trp Leu Val Leu		
245	250	255
Arg Ala Pro Arg Gly Gly Ala Gln Thr Pro Leu Tyr Cys Ala Leu		
260	265	270
Gln Glu Gly Ile Glu Pro Leu Ser Gly Arg Tyr Phe Ala Asn Cys		
275	280	285
His Val Glu Glu Val Pro Pro Ala Ala Arg Asp Asp Arg Ala Ala		
290	295	300
His Arg Leu Trp Glu Ala Ser Lys Arg Leu Ala Gly Leu Gly Pro		
305	310	315
Gly Glu Asp Ala Glu Pro Asp Glu Asp Pro Gln Ser Glu Asp Ser		
320	325	330
Glu Ala Pro Ser Ser Leu Ser Thr Pro His Pro Glu Glu Pro Thr		
335	340	345
Val Ser Gln Pro Tyr Pro Ser Pro Gln Ser Ser Pro Asp Leu Ser		
350	355	360
Lys Met Thr His Arg Ile Gln Ala Lys Val Glu Pro Glu Ile Gln		
365	370	375

Leu Ser

<210> 207

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 207

cttcatggcc ttgacttg ccag 24

<210> 208

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 208

acgccagtgg cctcaagctg gttg 24

<210> 209

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 209

ctttctgagc tctgagccac ggttggaat cctcatccac aatgc 45

<210> 210

<211> 3716

<212> DNA

<213> Homo sapiens

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<211> 985  
<212> PRT  
<213> Homo sapiens

<400> 211  
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20 25 30  
Cys Gln Ala Ser Gly Gln Pro Pro Pro Thr Ile Arg Trp Leu Leu  
35 40 45  
Asn Gly Gln Pro Leu Ser Met Val Pro Pro Asp Pro His His Leu  
50 55 60  
Leu Pro Asp Gly Thr Leu Leu Leu Leu Gln Pro Pro Ala Arg Gly  
65 70 75  
His Ala His Asp Gly Gln Ala Leu Ser Thr Asp Leu Gly Val Tyr  
80 85 90  
Thr Cys Glu Ala Ser Asn Arg Leu Gly Thr Ala Val Ser Arg Gly  
95 100 105  
Ala Arg Leu Ser Val Ala Val Leu Arg Glu Asp Phe Gln Ile Gln  
110 115 120  
Pro Arg Asp Met Val Ala Val Val Gly Glu Gln Phe Thr Leu Glu  
125 130 135  
Cys Gly Pro Pro Trp Gly His Pro Glu Pro Thr Val Ser Trp Trp  
140 145 150  
Lys Asp Gly Lys Pro Leu Ala Leu Gln Pro Gly Arg His Thr Val  
155 160 165  
Ser Gly Gly Ser Leu Leu Met Ala Arg Ala Glu Lys Ser Asp Glu  
170 175 180  
Gly Thr Tyr Met Cys Val Ala Thr Asn Ser Ala Gly His Arg Glu  
185 190 195

Ser Arg Ala Ala Arg Val Ser Ile Gln Glu Pro Gln Asp Tyr Thr  
200 205 210

Glu Pro Val Glu Leu Leu Ala Val Arg Ile Gln Leu Glu Asn Val  
215 220 225

Thr Leu Leu Asn Pro Asp Pro Ala Glu Gly Pro Lys Pro Arg Pro  
230 235 240

Ala Val Trp Leu Ser Trp Lys Val Ser Gly Pro Ala Ala Pro Ala  
245 250 255

Gln Ser Tyr Thr Ala Leu Phe Arg Thr Gln Thr Ala Pro Gly Gly  
260 265 270

Gln Gly Ala Pro Trp Ala Glu Glu Leu Leu Ala Gly Trp Gln Ser  
275 280 285

Ala Glu Leu Gly Gly Leu His Trp Gly Gln Asp Tyr Glu Phe Lys  
290 295 300

Val Arg Pro Ser Ser Gly Arg Ala Arg Gly Pro Asp Ser Asn Val  
305 310 315

Leu Leu Leu Arg Leu Pro Glu Lys Val Pro Ser Ala Pro Pro Gln  
320 325 330

Glu Val Thr Leu Lys Pro Gly Asn Gly Thr Val Phe Val Ser Trp  
335 340 345

Val Pro Pro Pro Ala Glu Asn His Asn Gly Ile Ile Arg Gly Tyr  
350 355 360

Gln Val Trp Ser Leu Gly Asn Thr Ser Leu Pro Pro Ala Asn Trp  
365 370 375

Thr Val Val Gly Glu Gln Thr Gln Leu Glu Ile Ala Thr His Met  
380 385 390

Pro Gly Ser Tyr Cys Val Gln Val Ala Ala Val Thr Gly Ala Gly  
395 400 405

Ala Gly Glu Pro Ser Arg Pro Val Cys Leu Leu Leu Glu Gln Ala  
410 415 420

Met Glu Arg Ala Thr Gln Glu Pro Ser Glu His Gly Pro Trp Thr  
425 430 435

Leu Glu Gln Leu Arg Ala Thr Leu Lys Arg Pro Glu Val Ile Ala  
440 445 450

Thr Cys Gly Val Ala Leu Trp Leu Leu Leu Gly Thr Ala Val  
455 460 465

Cys Ile His Arg Arg Arg Arg Ala Arg Val His Leu Gly Pro Gly  
470 475 480

Leu Tyr Arg Tyr Thr Ser Glu Asp Ala Ile Leu Lys His Arg Met  
485 490 495

Asp His Ser Asp Ser Gln Trp Leu Ala Asp Thr Trp Arg Ser Thr  
500 505 510

Ser Gly Ser Arg Asp Leu Ser Ser Ser Ser Ser Leu Ser Ser Arg  
515 520 525

Leu Gly Ala Asp Ala Arg Asp Pro Leu Asp Cys Arg Arg Ser Leu  
530 535 540

Leu Ser Trp Asp Ser Arg Ser Pro Gly Val Pro Leu Leu Pro Asp  
545 550 555

Thr Ser Thr Phe Tyr Gly Ser Leu Ile Ala Glu Leu Pro Ser Ser  
560 565 570

Thr Pro Ala Arg Pro Ser Pro Gln Val Pro Ala Val Arg Arg Leu  
575 580 585

Pro Pro Gln Leu Ala Gln Leu Ser Ser Pro Cys Ser Ser Ser Asp  
590 595 600

Ser Leu Cys Ser Arg Arg Gly Leu Ser Ser Pro Arg Leu Ser Leu  
605 610 615

Ala Pro Ala Glu Ala Trp Lys Ala Lys Lys Lys Gln Glu Leu Gln  
620 625 630

His Ala Asn Ser Ser Pro Leu Leu Arg Gly Ser His Ser Leu Glu  
635 640 645



Leu Arg Ala Cys Glu Leu Gly Asn Arg Gly Ser Lys Asn Leu Ser  
650 655 660

Gln Ser Pro Gly Ala Val Pro Gln Ala Leu Val Ala Trp Arg Ala  
665 670 675

Leu Gly Pro Lys Leu Leu Ser Ser Ser Asn Glu Leu Val Thr Arg  
680 685 690

His Leu Pro Pro Ala Pro Leu Phe Pro His Glu Thr Pro Pro Thr  
695 700 705

Gln Ser Gln Gln Thr Gln Pro Pro Val Ala Pro Gln Ala Pro Ser  
710 715 720

Ser Ile Leu Leu Pro Ala Ala Pro Ile Pro Ile Leu Ser Pro Cys  
725 730 735

Ser Pro Pro Ser Pro Gln Ala Ser Ser Leu Ser Gly Pro Ser Pro  
740 745 750

Ala Ser Ser Arg Leu Ser Ser Ser Ser Leu Ser Ser Leu Gly Glu  
755 760 765

Asp Gln Asp Ser Val Leu Thr Pro Glu Glu Val Ala Leu Cys Leu  
770 775 780

Glu Leu Ser Glu Gly Glu Glu Thr Pro Arg Asn Ser Val Ser Pro  
785 790 795

Met Pro Arg Ala Pro Ser Pro Pro Thr Thr Tyr Gly Tyr Ile Ser  
800 805 810

Val Pro Thr Ala Ser Glu Phe Thr Asp Met Gly Arg Thr Gly Gly  
815 820 825

Gly Val Gly Pro Lys Gly Gly Val Leu Leu Cys Pro Pro Arg Pro  
830 835 840

Cys Leu Thr Pro Thr Pro Ser Glu Gly Ser Leu Ala Asn Gly Trp  
845 850 855

Gly Ser Ala Ser Glu Asp Asn Ala Ala Ser Ala Arg Ala Ser Leu  
860 865 870

Val Ser Ser Ser Asp Gly Ser Phe Leu Ala Asp Ala His Phe Ala  
875 880 885

Arg Ala Leu Ala Val Ala Val Asp Ser Phe Gly Phe Gly Leu Glu  
890 895 900

Pro Arg Glu Ala Asp Cys Val Phe Ile Asp Ala Ser Ser Pro Pro  
905 910 915

Ser Pro Arg Asp Glu Ile Phe Leu Thr Pro Asn Leu Ser Leu Pro  
920 925 930

Leu Trp Glu Trp Arg Pro Asp Trp Leu Glu Asp Met Glu Val Ser  
935 940 945

His Thr Gln Arg Leu Gly Arg Gly Met Pro Pro Trp Pro Pro Asp  
950 955 960

Ser Gln Ile Ser Ser Gln Arg Ser Gln Leu His Cys Arg Met Pro  
965 970 975

Lys Ala Gly Ala Ser Pro Val Asp Tyr Ser  
980 985

<210> 212

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 212

gaagggacct acatgtgtgt ggcc 24

<210> 213

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 213

actgaccttc cagctgagcc acac 24

<210> 214  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 214  
aggactacac ggagcctgtg gagcttctgg ctgtgcgaat tcagctggaa 50

<210> 215  
<211> 2749  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 1869, 1887  
<223> unknown base

<400> 215  
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gcgggttcga aggggacact gtgtccctgc agtgcaccta caggaagag 150  
  
ctgagggacc accggaagta ctggtgcagg aagggtggga tcctcttctc 200  
  
tcgctgctct ggccacctct atgcagaaga agaaggccag gagacaatga 250  
  
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accctgtgga acctcaccct gcaagacgct ggggagtact ggtgtggggt 350  
  
cgaaaaacgg ggccccgatg agtctttact gatctctctg ttcgtcttc 400  
  
caggaccctg ctgtctccc tccccttctc ccaccttcca gcctctggct 450  
  
acaacacgcc tgcagcccaa ggcaaaagct cagcaaacc agccccagg 500  
  
attgacttct cctgggctct acccggcagc caccacagcc aagcagggga 550  
  
agacaggggc tgaggcccct ccattgccag ggacttccca gtacgggcac 600

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aggacaccag tccagctctc agcagtggca gctctaagcc cagggtgtcc 750  
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cagtgaagca gtatggctgg ctggatcagc accgattccc gaaagcttct 1100  
cacctcagcc tcagagtcca gctgcccgga ctccagggt ctccccacc 1150  
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cagcagggcc agacaaggt cagtggatct ggtctgagtt tcaatctgcc 1350  
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tcaccttat cgttcatca cttattcca gcacttct gtgtttaca 2700  
gacctttta taaataaaat gtcatcagc tgcataaaaa aaaaaaaaa 2749

<210> 216

<211> 332

<212> PRT

<213> Homo sapiens

<400> 216

Met Arg Leu Leu Val Leu Leu Trp Gly Cys Leu Leu Leu Pro Gly  
1 5 10 15

Tyr Glu Ala Leu Glu Gly Pro Glu Glu Ile Ser Gly Phe Glu Gly  
20 25 30

Asp Thr Val Ser Leu Gln Cys Thr Tyr Arg Glu Glu Leu Arg Asp  
35 40 45

His Arg Lys Tyr Trp Cys Arg Lys Gly Gly Ile Leu Phe Ser Arg  
50 55 60

Cys Ser Gly Thr Ile Tyr Ala Glu Glu Glu Gly Gln Glu Thr Met  
65 70 75

Lys Gly Arg Val Ser Ile Arg Asp Ser Arg Gln Glu Leu Ser Leu  
80 85 90

Ile Val Thr Leu Trp Asn Leu Thr Leu Gln Asp Ala Gly Glu Tyr  
95 100 105

Trp Cys Gly Val Glu Lys Arg Gly Pro Asp Glu Ser Leu Leu Ile  
110 115 120

Ser Leu Phe Val Phe Pro Gly Pro Cys Cys Pro Pro Ser Pro Ser  
125 130 135

Pro Thr Phe Gln Pro Leu Ala Thr Thr Arg Leu Gln Pro Lys Ala  
140 145 150

Lys Ala Gln Gln Thr Gln Pro Pro Gly Leu Thr Ser Pro Gly Leu  
155 160 165

Tyr Pro Ala Ala Thr Thr Ala Lys Gln Gly Lys Thr Gly Ala Glu  
170 175 180

Ala Pro Pro Leu Pro Gly Thr Ser Gln Tyr Gly His Glu Arg Thr  
185 190 195

Ser Gln Tyr Thr Gly Thr Ser Pro His Pro Ala Thr Ser Pro Pro  
200 205 210

Ala Gly Ser Ser Arg Pro Pro Met Gln Leu Asp Ser Thr Ser Ala  
215 220 225

Glu Asp Thr Ser Pro Ala Leu Ser Ser Gly Ser Ser Lys Pro Arg  
230 235 240

Val Ser Ile Pro Met Val Arg Ile Leu Ala Pro Val Leu Val Leu  
245 250 255

Leu Ser Leu Leu Ser Ala Ala Gly Leu Ile Ala Phe Cys Ser His  
260 265 270

Leu Leu Leu Trp Arg Lys Glu Ala Gln Gln Ala Thr Glu Thr Gln  
275 280 285

Arg Asn Glu Lys Phe Trp Leu Ser Arg Leu Thr Ala Glu Glu Lys  
290 295 300

Glu Ala Pro Ser Gln Ala Pro Glu Gly Asp Val Ile Ser Met Pro  
305 310 315

Pro Leu His Thr Ser Glu Glu Glu Leu Gly Phe Ser Lys Phe Val  
320 325 330

Ser Ala

<210> 217

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 217

ccctgcagtg cacctacagg gaag 24

<210> 218

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 218

ctgtcttccc ctgcttggt gtgg 24

<210> 219

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 219

ggtgcaggaa ggggtgggac ctcttctctc gctgctctgg ccacatc 47

<210> 220

<211> 950

<212> DNA

<213> Homo sapiens

<400> 220

tttgactaa aagctggcct agcaggccag ggagtgcagc tgcaggcgtg 50

gggggtggcag gagccgcaga gccagagcag acagccgaga aacaggtgga 100

cagtgtgaaa gaaccagtgg tctcgctctg ttgccaggc tagagtgtac 150

tggcgtgac atagctcact gcagcctcag actcctggac ttgagaaac 200

ctcctgcctt agcctcctgc atatctggga ctccaggggt gcactcaagc 250

cctgtttctt ctcttctgt gagtggacca cggaggctgg tgagctgcct 300

gtcatcccaa agctcagctc tgagccagag tgggtgtggc tccaccttg 350

ccgccggcat agaagccagg agcagggtc tcagaaggcg gtggtgcca 400

gctgggatca tgttgtggc cctggtctgt ctgctcagct gcctgtacc 450

ctccagttag gccaagctct acggtcgttg tgaactggcc agagtgtac 500

atgacttcgg gctggacgga taccggggat acagcctggc tgactgggtc 550

tgccttgctt attcacaag cggtttcaac gcagctgctt tggactacga 600

ggctgatggg agcaccaaca acgggatctt ccagatcaac agccggaggt 650

ggtgcagcaa cctcaccg aacgtccca acgtgtgccg gatgtactgc 700



tcagatttgt tgaatcctaa tctcaaggat accgttatct gtgccatgaa 750  
gataacccaa gagcctcagg gtctgggtta ctgggaggcc tggaggcatc 800  
actgccaggg aaaagacctc actgaatggg tggatggctg tgacttctag 850  
gatggacgga accatgcaca gcaggctggg aaatgtggtt tggttcctga 900  
cctaggcttg ggaagacaag ccagcgaata aaggatggtt gaacgtgaaa 950

<210> 221

<211> 146

<212> PRT

<213> Homo sapiens

<400> 221

Met Leu Leu Ala Leu Val Cys Leu Leu Ser Cys Leu Leu Pro Ser  
1 5 10 15

Ser Glu Ala Lys Leu Tyr Gly Arg Cys Glu Leu Ala Arg Val Leu  
20 25 30

His Asp Phe Gly Leu Asp Gly Tyr Arg Gly Tyr Ser Leu Ala Asp  
35 40 45

Trp Val Cys Leu Ala Tyr Phe Thr Ser Gly Phe Asn Ala Ala Ala  
50 55 60

Leu Asp Tyr Glu Ala Asp Gly Ser Thr Asn Asn Gly Ile Phe Gln  
65 70 75

Ile Asn Ser Arg Arg Trp Cys Ser Asn Leu Thr Pro Asn Val Pro  
80 85 90

Asn Val Cys Arg Met Tyr Cys Ser Asp Leu Leu Asn Pro Asn Leu  
95 100 105

Lys Asp Thr Val Ile Cys Ala Met Lys Ile Thr Gln Glu Pro Gln  
110 115 120

Gly Leu Gly Tyr Trp Glu Ala Trp Arg His His Cys Gln Gly Lys  
125 130 135

Asp Leu Thr Glu Trp Val Asp Gly Cys Asp Phe  
140 145

<210> 222

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 222

gggatcatgt tgttggccct ggtc 24

<210> 223

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 223

gcaaggcaga ccagtcagc cag 23

<210> 224

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 224

ctgcctgcta cctccaagt gaggccaagc tctacggtcg ttgtg 45

<210> 225

<211> 2049

<212> DNA

<213> Homo sapiens

<400> 225

agccgctgcc ccgggccggg cgcccgcggc ggcaccatga gtccccgctc 50

gtgcctgcgt tcgtgcgcc tcctcgtctt cgccgtcttc tcagccgccg 100

cgagcaactg gctgtacctg gccaaagtgt cgtcgggtggg gagcatctca 150

gaggaggaga cgtgcgagaa actcaagggc ctgatccaga ggcaggtgca 200  
gatgtgcaag cggaacctgg aagtcatgga ctcggtgcgc cgcggtgccc 250  
agctggccat tgaggagtgc cagtaccagt tccggaaccg gcgctggaac 300  
tgctccacac tcgactcctt gcccgtcttc ggcaaggtgg tgacgcaagg 350  
gactcgggag gcggccttcg tgtacgcat ctctcggca ggtgtggcct 400  
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gacaggacag tgcatggggg cagcccacag ggcttcagt ggtcaggatg 500  
ctctgacaac atgcctacg gtgtggcctt ctacagtcg tttgtgatg 550  
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 catgaaactg aaaaacacac acacacacac acacacacac acacacacac 1950  
 acacacacac ggacacacac acacacctgc gagagagagg gaggaaaggg 2000  
 ctgtgccttt gcagtcatgc ccgagtcacc tttcacagca ctgttcctc 2049

<210> 226

<211> 351

<212> PRT

<213> Homo sapiens

<400> 226

Met	Ser	Pro	Arg	Ser	Cys	Leu	Arg	Ser	Leu	Arg	Leu	Leu	Val	Phe
1		5				10					15			

Ala	Val	Phe	Ser	Ala	Ala	Ala	Ser	Asn	Trp	Leu	Tyr	Leu	Ala	Lys
			20				25						30	

Leu	Ser	Ser	Val	Gly	Ser	Ile	Ser	Glu	Glu	Glu	Thr	Cys	Glu	Lys
				35			40						45	

Leu Lys Gly Leu Ile Gln Arg Gln Val Gln Met Cys Lys Arg Asn  
50 55 60

Leu Glu Val Met Asp Ser Val Arg Arg Gly Ala Gln Leu Ala Ile  
65 70 75

Glu Glu Cys Gln Tyr Gln Phe Arg Asn Arg Arg Trp Asn Cys Ser  
80 85 90

Thr Leu Asp Ser Leu Pro Val Phe Gly Lys Val Val Thr Gln Gly  
95 100 105

Thr Arg Glu Ala Ala Phe Val Tyr Ala Ile Ser Ser Ala Gly Val  
110 115 120

Ala Phe Ala Val Thr Arg Ala Cys Ser Ser Gly Glu Leu Glu Lys  
125 130 135

Cys Gly Cys Asp Arg Thr Val His Gly Val Ser Pro Gln Gly Phe  
140 145 150

Gln Trp Ser Gly Cys Ser Asp Asn Ile Ala Tyr Gly Val Ala Phe  
155 160 165

Ser Gln Ser Phe Val Asp Val Arg Glu Arg Ser Lys Gly Ala Ser  
170 175 180

Ser Ser Arg Ala Leu Met Asn Leu His Asn Asn Glu Ala Gly Arg  
185 190 195

Lys Ala Ile Leu Thr His Met Arg Val Glu Cys Lys Cys His Gly  
200 205 210

Val Ser Gly Ser Cys Glu Val Lys Thr Cys Trp Arg Ala Val Pro  
215 220 225

Pro Phe Arg Gln Val Gly His Ala Leu Lys Glu Lys Phe Asp Gly  
230 235 240

Ala Thr Glu Val Glu Pro Arg Arg Val Gly Ser Ser Arg Ala Leu  
245 250 255

Val Pro Arg Asn Ala Gln Phe Lys Pro His Thr Asp Glu Asp Leu  
260 265 270

Val Tyr Leu Glu Pro Ser Pro Asp Phe Cys Glu Gln Asp Met Arg  
275 280 285

Ser Gly Val Leu Gly Thr Arg Gly Arg Thr Cys Asn Lys Thr Ser  
290 295 300

Lys Ala Ile Asp Gly Cys Glu Leu Leu Cys Cys Gly Arg Gly Phe  
305 310 315

His Thr Ala Gln Val Glu Leu Ala Glu Arg Cys Ser Cys Lys Phe  
320 325 330

His Trp Cys Cys Phe Val Lys Cys Arg Gln Cys Gln Arg Leu Val  
335 340 345

Glu Leu His Thr Cys Arg  
350

<210> 227

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 227

gctgcagctg caaatccac tgg 23

<210> 228

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 228

tggtgggaga ctgtttaa ttcggcc 28

<210> 229

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 229

tgcttcgtca agtcccggca gtgccagcgg ctcgtggagt t 41

<210> 230

<211> 1355

<212> DNA

<213> Homo sapiens

<400> 230

cggacgcgtg ggccggacgc tgggcggacg cgtgggcgga cgcgtgggct 50

gggtgcctgc atgccatgg acaccaccag gtacagcaag tggggcggca 100

gctccgagga ggtccccgga gggccctggg gacgctgggt gcactggagc 150

aggagacccc tcttcttggc cctggctgtc ctggtcacca cagtcctttg 200

ggctgtgatt ctgagtatcc tattgtcaa ggccctccac gagcgcgcgg 250

cgctgcttga cggccacgac ctgctgagga caaacgcctc gaagcagacg 300

gcggcgctgg gtgccctgaa ggaggaggct ggagactgcc acagctgctg 350

ctcggggacg caggcgcagc tgcagaccac gcgcgcggag ctggggagg 400

cgcaggcgaa gctgatggag caggagagcg ccctgcggga actgcgtgag 450

cgcgtgaccc agggcttggc tgaagccggc aggggcccgt aggacgtccg 500

cactgagctg ttccgggcgc tggaggccgt gaggtccag aacaactcct 550

gcgagccgtg cccacgtcg tggctgtcct tcgagggtc ctgtacttt 600

ttctctgtgc caaagacgac gtgggcggcg gcgcaggatc actgcgcaga 650

tgccagcgcg cacctggtga tcgttggggg cctggatgag cagggttcc 700

tcactcgga cagcgtggc cgtggttact ggctgggcct gagggctgtg 750

cgccatctgg gcaaggttca gggctaccag tgggtggacg gagtctctt 800

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 gtgactgagg actggagctg ttggttttc tcgcatttc caccaaactg 1300  
 gaagctgttt ttgcagcctg aggaagcatc aataaatatt tgagaaatga 1350  
 aaaaa 1355

<210> 231  
 <211> 293  
 <212> PRT  
 <213> Homo sapiens

<400> 231  
 Met Asp Thr Thr Arg Tyr Ser Lys Trp Gly Gly Ser Ser Glu Glu  
 1 5 10 15  
 Val Pro Gly Gly Pro Trp Gly Arg Trp Val His Trp Ser Arg Arg  
 20 25 30  
 Pro Leu Phe Leu Ala Leu Ala Val Leu Val Thr Thr Val Leu Trp  
 35 40 45  
 Ala Val Ile Leu Ser Ile Leu Leu Ser Lys Ala Ser Thr Glu Arg  
 50 55 60  
 Ala Ala Leu Leu Asp Gly His Asp Leu Leu Arg Thr Asn Ala Ser  
 65 70 75  
 Lys Gln Thr Ala Ala Leu Gly Ala Leu Lys Glu Glu Val Gly Asp  
 80 85 90



Cys His Ser Cys Cys Ser Gly Thr Gln Ala Gln Leu Gln Thr Thr  
95 100 105

Arg Ala Glu Leu Gly Glu Ala Gln Ala Lys Leu Met Glu Gln Glu  
110 115 120

Ser Ala Leu Arg Glu Leu Arg Glu Arg Val Thr Gln Gly Leu Ala  
125 130 135

Glu Ala Gly Arg Gly Arg Glu Asp Val Arg Thr Glu Leu Phe Arg  
140 145 150

Ala Leu Glu Ala Val Arg Leu Gln Asn Asn Ser Cys Glu Pro Cys  
155 160 165

Pro Thr Ser Trp Leu Ser Phe Glu Gly Ser Cys Tyr Phe Phe Ser  
170 175 180

Val Pro Lys Thr Thr Trp Ala Ala Ala Gln Asp His Cys Ala Asp  
185 190 195

Ala Ser Ala His Leu Val Ile Val Gly Gly Leu Asp Glu Gln Gly  
200 205 210

Phe Leu Thr Arg Asn Thr Arg Gly Arg Gly Tyr Trp Leu Gly Leu  
215 220 225

Arg Ala Val Arg His Leu Gly Lys Val Gln Gly Tyr Gln Trp Val  
230 235 240

Asp Gly Val Ser Leu Ser Phe Ser His Trp Asn Gln Gly Glu Pro  
245 250 255

Asn Asp Ala Trp Gly Arg Glu Asn Cys Val Met Met Leu His Thr  
260 265 270

Gly Leu Trp Asn Asp Ala Pro Cys Asp Ser Glu Lys Asp Gly Trp  
275 280 285

Ile Cys Glu Lys Arg His Asn Cys  
290

<210> 232

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 232

gcgagaactg tgcatgatg ctgc 24

<210> 233

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 233

gtttctgaga ctcagcagcg gtgg 24

<210> 234

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 234

caccgtgtga cagcgagaag gacggctgga tctgtgagaa aaggcacaac 50

<210> 235

<211> 1847

<212> DNA

<213> Homo sapiens

<400> 235

gccaggggaa gagggatgac cgacccgggg aaggctcgtg ggcagggcga 50

gttgggaaag cggcagcccc cgccgcccc gcagcccctt ctctccttt 100

ctccacgtc ctatctgct ctcgctggag gccaggccgt gcagcatga 150

agacaggagg aactggagcc tcattggccg gcccggggcg ccggcctcgg 200

gcttaaatag gagctccggg ctctggctgg gacccgaccg ctgccggccg 250

cgctcccgt gctcctgccg ggtgatggaa aaccccagcc cggccgccgc 300  
cctgggcaag gccctctgcg ctctctctct ggccactctc ggcgccgccg 350  
gccagcctct tgggggagag tccatctgtt ccgccagagc cccggccaaa 400  
tacagcatca ccttcacggg caagtggagc cagacggcct tcccaagca 450  
gtacccctg ttccgcccc ctgcgcagtg gtcttcgtg ctgggggccg 500  
cgcatagctc cgactacagc atgtggagga agaaccagta cgtcagtaac 550  
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tcctgataa ctgcgtctaa gaccagagcc ccgagcccc tggggcccc 1300  
cggagccatg ggggtgcggg ggctcctgtg caggctcatg ctgcaggcgg 1350  
ccgagggcac aggggggttc gcgtgtctc tgaccgcgtt gaggccgcgc 1400

cgaccatctc tgcactgaag ggccctctgg tggccggcac' gggcattggg 1450

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gtctgtctc agcctctccc tctgcagga taaagtcac cccaaggctc 1550

cagctactct aaattatgtc tccttataag ttattgctgc tccaggagat 1600

tgtccttcat cgtccagggg cctggctccc acgtggtgc agatacctca 1650

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agcgggggcc acttgagaag tgaataaatg gggcggttgc ggaagcgtca 1750

gtgtttccat gttatggatc tctctcggtt tgaataaaga ctatctctgt 1800

tgctcacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1847

<210> 236

<211> 331

<212> PRT

<213> Homo sapiens

<400> 236

Met Glu Asn Pro Ser Pro Ala Ala Ala Leu Gly Lys Ala Leu Cys

1 5 10 15

Ala Leu Leu Leu Ala Thr Leu Gly Ala Ala Gly Gln Pro Leu Gly

20 25 30

Gly Glu Ser Ile Cys Ser Ala Arg Ala Pro Ala Lys Tyr Ser Ile

35 40 45

Thr Phe Thr Gly Lys Trp Ser Gln Thr Ala Phe Pro Lys Gln Tyr

50 55 60

Pro Leu Phe Arg Pro Pro Ala Gln Trp Ser Ser Leu Leu Gly Ala

65 70 75

Ala His Ser Ser Asp Tyr Ser Met Trp Arg Lys Asn Gln Tyr Val

80 85 90

Ser Asn Gly Leu Arg Asp Phe Ala Glu Arg Gly Glu Ala Trp Ala

95 100 105

Leu Met Lys Glu Ile Glu Ala Ala Gly Glu Ala Leu Gln Ser Val  
110 115 120

His Glu Val Phe Ser Ala Pro Ala Val Pro Ser Gly Thr Gly Gln  
125 130 135

Thr Ser Ala Glu Leu Glu Val Gln Arg Arg His Ser Leu Val Ser  
140 145 150

Phe Val Val Arg Ile Val Pro Ser Pro Asp Trp Phe Val Gly Val  
155 160 165

Asp Ser Leu Asp Leu Cys Asp Gly Asp Arg Trp Arg Glu Gln Ala  
170 175 180

Ala Leu Asp Leu Tyr Pro Tyr Asp Ala Gly Thr Asp Ser Gly Phe  
185 190 195

Thr Phe Ser Ser Pro Asn Phe Ala Thr Ile Pro Gln Asp Thr Val  
200 205 210

Thr Glu Ile Thr Ser Ser Ser Pro Ser His Pro Ala Asn Ser Phe  
215 220 225

Tyr Tyr Pro Arg Leu Lys Ala Leu Pro Pro Ile Ala Arg Val Thr  
230 235 240

Leu Leu Arg Leu Arg Gln Ser Pro Arg Ala Phe Ile Pro Pro Ala  
245 250 255

Pro Val Leu Pro Ser Arg Asp Asn Glu Ile Val Asp Ser Ala Ser  
260 265 270

Val Pro Glu Thr Pro Leu Asp Cys Glu Val Ser Leu Trp Ser Ser  
275 280 285

Trp Gly Leu Cys Gly Gly His Cys Gly Arg Leu Gly Thr Lys Ser  
290 295 300

Arg Thr Arg Tyr Val Arg Val Gln Pro Ala Asn Asn Gly Ser Pro  
305 310 315

Cys Pro Glu Leu Glu Glu Glu Ala Glu Cys Val Pro Asp Asn Cys  
320 325 330

Val

<210> 237

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 237

cagcactgcc aggggaagag gg 22

<210> 238

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 238

caggactcgc tacgtccg 18

<210> 239

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 239

cagcccttc tcctctttc tccc 24

<210> 240

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 240

gcagttatca gggacgcact cagcc 25

<210> 241

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 241

ccagcgagag gcagatag 18

<210> 242

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 242

cggtcaccgt gtctgcggg atg 23

<210> 243

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 243

cagcccttc tctccttc tcccagtc tatctgcctc tc 42

<210> 244

<211> 1894

<212> DNA

<213> Homo sapiens

<400> 244

ggcggcgctc gtgaggggct ccttgggca ggggtagtgt ttggtgtccc 50

tgtcttgcgt gatattgaca aactgaagct ttctgcacc actggactta 100

aggaagagtg tactcgtagg cggacagctt tagtggccgg cggccgctc 150  
tcacccccg taaggagcag agtcctttgt actgaccaag atgagcaaca 200  
tctacatcca ggagcctccc acgaatggga aggttttatt gaaaactaca 250  
gctggagata ttgacataga gttgtgggcc aaagaagctc ctaaagcttg 300  
cagaaattti atccaacttt gtttgaagc ttattatgac aataccattt 350  
ttcatagagt tgtgcctggt ttcatagtcc aaggcggaga tcctactggc 400  
acagggagtg gtggagagtc tatctatgga gcgccattca aagatgaatt 450  
tcattcacgg ttgcgtttta atcggagagg actggttgcc atggcaaatg 500  
ctggttctca tgataatggc agccagtttt tcttcacact gggtcgagca 550  
gatgaactta acaataagca taccatcttt ggaaaggta caggggatac 600  
agtatataac atgttgcgac tgtcagaagt agacattgat gatgacgaaa 650  
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tttgatgaca tcattccaag ggaaattaaa aggctgaaaa aagagaaacc 750  
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atgcaccaga tttagttgat gatggagaag atgaaagtgc agagcatgat 1000  
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aaaattaaaa aaggacacaa gtgcgaatgt taaatcagct ggagaaggag 1100  
aagtggagaa gaaatcagtc agccgcagtg aagagctcag aaaagaagca 1150  
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 actgctgaac cagttaaataa ctaaactcac tcaagcaatt gctgaaacac 1400  
 ctgaaaatga cattcctgaa acagaagtag aagatgatga aggatggatg 1450  
 tcacatgtac ttcagtttga ggataaaaagc agaaaagtga aagatgcaag 1500  
 catgcaagac tcagatacat ttgaaatcta tgatcctcgg aatccagtga 1550  
 ataaaagaag gagggaagaa agcaaaaagc tgatgagaga gaaaaaagaa 1600  
 agaagataaa atgagaataa tgataaccag aacttgctgg aaatgtgcct 1650  
 acaatggcct tgtaacagcc attgttccca acagcatcac ttaggggtgt 1700  
 gaaaagaagt attttgaac ctgtgtctg gtttgaaaa acaattatct 1750  
 tgttttcaa attgtggaat gatgtaagca aatgctttg gttactggta 1800  
 catgtgtttt ttctagctg accttttata ttgctaaatc tgaaataaaa 1850  
 taactttcct tccacaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1894

<210> 245  
 <211> 472  
 <212> PRT  
 <213> Homo sapiens

<400> 245  
 Met Ser Asn Ile Tyr Ile Gln Glu Pro Pro Thr Asn Gly Lys Val  
 1 5 10 15  
 Leu Leu Lys Thr Thr Ala Gly Asp Ile Asp Ile Glu Leu Trp Ser  
 20 25 30  
 Lys Glu Ala Pro Lys Ala Cys Arg Asn Phe Ile Gln Leu Cys Leu  
 35 40 45  
 Glu Ala Tyr Tyr Asp Asn Thr Ile Phe His Arg Val Val Pro Gly  
 50 55 60  
 Phe Ile Val Gln Gly Gly Asp Pro Thr Gly Thr Gly Ser Gly Gly

65	70	75
Glu Ser Ile Tyr Gly Ala Pro Phe Lys Asp Glu Phe His Ser Arg		
80	85	90
Leu Arg Phe Asn Arg Arg Gly Leu Val Ala Met Ala Asn Ala Gly		
95	100	105
Ser His Asp Asn Gly Ser Gln Phe Phe Phe Thr Leu Gly Arg Ala		
110	115	120
Asp Glu Leu Asn Asn Lys His Thr Ile Phe Gly Lys Val Thr Gly		
125	130	135
Asp Thr Val Tyr Asn Met Leu Arg Leu Ser Glu Val Asp Ile Asp		
140	145	150
Asp Asp Glu Arg Pro His Asn Pro His Lys Ile Lys Ser Cys Glu		
155	160	165
Val Leu Phe Asn Pro Phe Asp Asp Ile Ile Pro Arg Glu Ile Lys		
170	175	180
Arg Leu Lys Lys Glu Lys Pro Glu Glu Glu Val Lys Lys Leu Lys		
185	190	195
Pro Lys Gly Thr Lys Asn Phe Ser Leu Leu Ser Phe Gly Glu Glu		
200	205	210
Ala Glu Glu Glu Glu Glu Glu Val Asn Arg Val Ser Gln Ser Met		
215	220	225
Lys Gly Lys Ser Lys Ser Ser His Asp Leu Leu Lys Asp Asp Pro		
230	235	240
His Leu Ser Ser Val Pro Val Val Glu Ser Glu Lys Gly Asp Ala		
245	250	255
Pro Asp Leu Val Asp Asp Gly Glu Asp Glu Ser Ala Glu His Asp		
260	265	270
Glu Tyr Ile Asp Gly Asp Glu Lys Asn Leu Met Arg Glu Arg Ile		
275	280	285
Ala Lys Lys Leu Lys Lys Asp Thr Ser Ala Asn Val Lys Ser Ala		

290	295	300
Gly Glu Gly Glu Val Glu Lys Lys Ser Val Ser Arg Ser Glu Glu		
305	310	315
Leu Arg Lys Glu Ala Arg Gln Leu Lys Arg Glu Leu Leu Ala Ala		
320	325	330
Lys Gln Lys Lys Val Glu Asn Ala Ala Lys Gln Ala Glu Lys Arg		
335	340	345
Ser Glu Glu Glu Glu Ala Pro Pro Asp Gly Ala Val Ala Glu Tyr		
350	355	360
Arg Arg Glu Lys Gln Lys Tyr Glu Ala Leu Arg Lys Gln Gln Ser		
365	370	375
Lys Lys Gly Thr Ser Arg Glu Asp Gln Thr Leu Ala Leu Leu Asn		
380	385	390
Gln Phe Lys Ser Lys Leu Thr Gln Ala Ile Ala Glu Thr Pro Glu		
395	400	405
Asn Asp Ile Pro Glu Thr Glu Val Glu Asp Asp Glu Gly Trp Met		
410	415	420
Ser His Val Leu Gln Phe Glu Asp Lys Ser Arg Lys Val Lys Asp		
425	430	435
Ala Ser Met Gln Asp Ser Asp Thr Phe Glu Ile Tyr Asp Pro Arg		
440	445	450
Asn Pro Val Asn Lys Arg Arg Arg Glu Glu Ser Lys Lys Leu Met		
455	460	465
Arg Glu Lys Lys Glu Arg Arg		
470		

<210> 246

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 246  
tgcggagatc ctactggcac aggg 24

<210> 247  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 247  
cgagttagtc agagcatg 18

<210> 248  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 248  
cagatggtgc tgttgccg 18

<210> 249  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 249  
caactggaac aggaactgag atgtggatc 29

<210> 250  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 250

ctgggtcagc agtgcaaggg tctg 24

<210> 251

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 251

cctctccgat taaaacgc 18

<210> 252

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 252

gagaggactg gttgcatgg caaatgctgg ttctcatgat aatgg 45

<210> 253

<211> 2456

<212> DNA

<213> Homo sapiens

<400> 253

cgccgccgtt ggggctggaa gttcccgcca ggtccgtgcc gggcgagaga 50

gatgtgccc ggcccgcctc ggctttgagg cgagagaagt gtcccagacc 100

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ttctcctcg ggtccgggac tctgggctcc accaccgtgg ccgccggcgg 200

gaccagcaca ggcggcggtt tctccttcgg aacgggaacg tctagcaacc 250

cttctgtggg gctcaatgtt ggaaatcttg gaagtacttc aactccagca 300

actacatctg ctcttcaag tggttttgga accgggctct ttgatctaa 350

acctgccact gggttcactc taggaggaac aaatacaggt gccttcaca 400

ccaagaggcc tcaagtggc accaaatag gaacctgca aggaaaacag 450  
atgcatgtgg ggaagacacc catccaagtc ttttaggag tccccttctc 500  
cagacctcct ctaggtatcc tcaggttgc acctccagaa cccccggagc 550  
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gttcggccag tcggcggggg ccatgagcat ctgaggactg atgatgtcac 1150  
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ttattcagac tttcatcac tagtaacca ctgaaagtgg ccaagaaggt 1250  
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gcctgagggc actatcagg accaaggtga tgcgtgtgc caacaagatg 1350  
agattcctcc aactgaactt ccagagagac ccggaagaga ttatctggtc 1400  
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 ttggatgag tctgtaccag tctcaaagac ctgagaagca gaggcaattc 1850  
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 caggccctgg ggagactagc catggacata cctggggaca agagttctac 1950  
 ccacccagtt ttagaactgc aggagctccc tgctgcctcc aggccaaagc 2000  
 tagagctttt gcctgtgtg tgggacctgc actgcccttt ccagcctgac 2050  
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 ctgtcaacac cacactgtgc tcagctctcc agcctcagga caacctctt 2150  
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 tggcctggag gcctagggca gggtgtgaca tggagcaaac ttttgtagt 2350  
 ttgggatctt ctctcccacc cacactatc tccccaggg ccactccaaa 2400  
 gtctatacac aggggtggtc tcttcaataa agaagtgtg attagaaaaa 2450  
 aaaaaa 2456

<210> 254

<211> 545

<212> PRT

<213> Homo sapiens

<400> 254

Met Ser Thr Gly Phe Ser Phe Gly Ser Gly Thr Leu Gly Ser Thr

1	5	10	15
Thr Val Ala Ala Gly Gly Thr Ser Thr Gly Gly Val Phe Ser Phe			
20	25	30	
Gly Thr Gly Thr Ser Ser Asn Pro Ser Val Gly Leu Asn Phe Gly			
35	40	45	
Asn Leu Gly Ser Thr Ser Thr Pro Ala Thr Thr Ser Ala Pro Ser			
50	55	60	
Ser Gly Phe Gly Thr Gly Leu Phe Gly Ser Lys Pro Ala Thr Gly			
65	70	75	
Phe Thr Leu Gly Gly Thr Asn Thr Gly Ala Leu His Thr Lys Arg			
80	85	90	
Pro Gln Val Val Thr Lys Tyr Gly Thr Leu Gln Gly Lys Gln Met			
95	100	105	
His Val Gly Lys Thr Pro Ile Gln Val Phe Leu Gly Val Pro Phe			
110	115	120	
Ser Arg Pro Pro Leu Gly Ile Leu Arg Phe Ala Pro Pro Glu Pro			
125	130	135	
Pro Glu Pro Trp Lys Gly Ile Arg Asp Ala Thr Thr Tyr Pro Pro			
140	145	150	
Gly Trp Ser Leu Ala Leu Ser Pro Gly Trp Ser Ala Val Ala Arg			
155	160	165	
Ser Arg Leu Thr Ala Thr Ser Ala Ser Arg Val Gln Ala Ser Leu			
170	175	180	
Leu Pro Gln Pro Leu Ser Val Trp Gly Tyr Arg Cys Leu Gln Glu			
185	190	195	
Ser Trp Gly Gln Leu Ala Ser Met Tyr Val Ser Thr Arg Glu Arg			
200	205	210	
Tyr Lys Trp Leu Arg Phe Ser Glu Asp Cys Leu Tyr Leu Asn Val			
215	220	225	
Tyr Ala Pro Ala Arg Ala Pro Gly Asp Pro Gln Leu Pro Val Met			



230	235	240
Val Trp Phe Pro Gly Gly Ala Phe Ile Val Gly Ala Ala Ser Ser		
245	250	255
Tyr Glu Gly Ser Asp Leu Ala Ala Arg Glu Lys Val Val Leu Val		
260	265	270
Phe Leu Gln His Arg Leu Gly Ile Phe Gly Phe Leu Ser Thr Asp		
275	280	285
Asp Ser His Ala Arg Gly Asn Trp Gly Leu Leu Asp Gln Met Ala		
290	295	300
Ala Leu Arg Trp Val Gln Glu Asn Ile Ala Ala Phe Gly Gly Asp		
305	310	315
Pro Gly Asn Val Thr Leu Phe Gly Gln Ser Ala Gly Ala Met Ser		
320	325	330
Ile Ser Gly Leu Met Met Ser Pro Leu Ala Ser Gly Leu Phe His		
335	340	345
Arg Ala Ile Ser Gln Ser Gly Thr Ala Leu Phe Arg Leu Phe Ile		
350	355	360
Thr Ser Asn Pro Leu Lys Val Ala Lys Lys Val Ala His Leu Ala		
365	370	375
Gly Cys Asn His Asn Ser Thr Gln Ile Leu Val Asn Cys Leu Arg		
380	385	390
Ala Leu Ser Gly Thr Lys Val Met Arg Val Ser Asn Lys Met Arg		
395	400	405
Phe Leu Gln Leu Asn Phe Gln Arg Asp Pro Glu Glu Ile Ile Trp		
410	415	420
Ser Met Ser Pro Val Val Asp Gly Val Val Ile Pro Asp Asp Pro		
425	430	435
Leu Val Leu Leu Thr Gln Gly Lys Val Ser Ser Val Pro Tyr Leu		
440	445	450
Leu Gly Val Asn Asn Leu Glu Phe Asn Trp Leu Leu Pro Tyr Asn		

455 460 465

Ile Thr Lys Glu Gln Val Pro Leu Val Val Glu Glu Tyr Leu Asp  
470 475 480

Asn Val Asn Glu His Asp Trp Lys Met Leu Arg Asn Arg Met Met  
485 490 495

Asp Ile Val Gln Asp Ala Thr Phe Val Tyr Ala Thr Leu Gln Thr  
500 505 510

Ala His Tyr His Arg Glu Thr Pro Met Met Gly Ile Cys Pro Ala  
515 520 525

Gly His Ala Thr Thr Arg Met Lys Ser Thr Cys Ser Trp Ile Leu  
530 535 540

Pro Gln Glu Trp Ala  
545

<210> 255

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 255

aggtgcctgc aggagtcctg ggg 23

<210> 256

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 256

ccacctcagg aagccgaaga tgcc 24

<210> 257

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 257

gaacgggtaca agtggctgcg cttcagcgag gactgtctgt acctg 45

<210> 258

<211> 2764

<212> DNA

<213> Homo sapiens

<400> 258

gagaacaggc ctgtctcagg caggccctgc gcctcctatg cggagatgct 50

actgccactg ctgctgtcct cgctgctggg cgggtcccag gctatggatg 100

ggagattctg gatacgagtg caggagtcag tgatgggtgcc ggagggcctg 150

tgcattcttg tgcctgtctc ttctcctac ccccgacaag actggacagg 200

gtctacccca gcttatggct actggttcaa agcagtgact gagacaacca 250

agggtgctcc tgtggccaca aaccaccaga gtcgagaggt ggaaatgagc 300

acccgggggcc gattccagct cactggggat cccgccaagg ggaactgctc 350

cttggtgatc agagacgcgc agatgcagga tgagtcacag tacttctttc 400

gggtggagag aggaagctat gtgacatata attcatgaa cgatgggttc 450

tttctaaaag taacagtgtc cagcttcacg cccagacccc aggaccacaa 500

caccgacctc acctgccatg tggacttctc cagaaagggt gtgagcgcac 550

agaggaccgt ccgactccgt gtggcctatg ccccagaga cttgtttatc 600

agcatttcac gtgacaacac gccagccctg gagccccagc cccagggaaa 650

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ctgctgacag ccagccccct gccacactga gctgggtcct gcagaacaga 750

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<210> 259

<211> 544

<212> PRT

<213> Homo sapiens

<400> 259

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25

30

Val Pro Glu Gly Leu Cys Ile Ser Val Pro Cys Ser Phe Ser Tyr  
35 40 45

Pro Arg Gln Asp Trp Thr Gly Ser Thr Pro Ala Tyr Gly Tyr Trp  
50 55 60

Phe Lys Ala Val Thr Glu Thr Thr Lys Gly Ala Pro Val Ala Thr  
65 70 75

Asn His Gln Ser Arg Glu Val Glu Met Ser Thr Arg Gly Arg Phe  
80 85 90

Gln Leu Thr Gly Asp Pro Ala Lys Gly Asn Cys Ser Leu Val Ile  
95 100 105

Arg Asp Ala Gln Met Gln Asp Glu Ser Gln Tyr Phe Phe Arg Val  
110 115 120

Glu Arg Gly Ser Tyr Val Thr Tyr Asn Phe Met Asn Asp Gly Phe  
125 130 135

Phe Leu Lys Val Thr Val Leu Ser Phe Thr Pro Arg Pro Gln Asp  
140 145 150

His Asn Thr Asp Leu Thr Cys His Val Asp Phe Ser Arg Lys Gly  
155 160 165

Val Ser Ala Gln Arg Thr Val Arg Leu Arg Val Ala Tyr Ala Pro  
170 175 180

Arg Asp Leu Val Ile Ser Ile Ser Arg Asp Asn Thr Pro Ala Leu  
185 190 195

Glu Pro Gln Pro Gln Gly Asn Val Pro Tyr Leu Glu Ala Gln Lys  
200 205 210

Gly Gln Phe Leu Arg Leu Leu Cys Ala Ala Asp Ser Gln Pro Pro  
215 220 225

Ala Thr Leu Ser Trp Val Leu Gln Asn Arg Val Leu Ser Ser Ser  
230 235 240

His Pro Trp Gly Pro Arg Pro Leu Gly Leu Glu Leu Pro Gly Val  
245 250 255

Lys Ala Gly Asp Ser Gly Arg Tyr Thr Cys Arg Ala Glu Asn Arg  
260 265 270

Leu Gly Ser Gln Gln Arg Ala Leu Asp Leu Ser Val Gln Tyr Pro  
275 280 285

Pro Glu Asn Leu Arg Val Met Val Ser Gln Ala Asn Arg Thr Val  
290 295 300

Leu Glu Asn Leu Gly Asn Gly Thr Ser Leu Pro Val Leu Glu Gly  
305 310 315

Gln Ser Leu Cys Leu Val Cys Val Thr His Ser Ser Pro Pro Ala  
320 325 330

Arg Leu Ser Trp Thr Gln Arg Gly Gln Val Leu Ser Pro Ser Gln  
335 340 345

Pro Ser Asp Pro Gly Val Leu Glu Leu Pro Arg Val Gln Val Glu  
350 355 360

His Glu Gly Glu Phe Thr Cys His Ala Arg His Pro Leu Gly Ser  
365 370 375

Gln His Val Ser Leu Ser Leu Ser Val His Tyr Lys Lys Gly Leu  
380 385 390

Ile Ser Thr Ala Phe Ser Asn Gly Ala Phe Leu Gly Ile Gly Ile  
395 400 405

Thr Ala Leu Leu Phe Leu Cys Leu Ala Leu Ile Ile Met Lys Ile  
410 415 420

Leu Pro Lys Arg Arg Thr Gln Thr Glu Thr Pro Arg Pro Arg Phe  
425 430 435

Ser Arg His Ser Thr Ile Leu Asp Tyr Ile Asn Val Val Pro Thr  
440 445 450

Ala Gly Pro Leu Ala Gln Lys Arg Asn Gln Lys Ala Thr Pro Asn  
455 460 465

Ser Pro Arg Thr Pro Pro Pro Gly Ala Pro Ser Pro Glu Ser  
470 475 480

Lys Lys Asn Gln Lys Lys Gln Tyr Gln Leu Pro Ser Phe Pro Glu  
485 490 495

Pro Lys Ser Ser Thr Gln Ala Pro Glu Ser Gln Glu Ser Gln Glu  
500 505 510

Glu Leu His Tyr Ala Thr Leu Asn Phe Pro Gly Val Arg Pro Arg  
515 520 525

Pro Glu Ala Arg Met Pro Lys Gly Thr Gln Ala Asp Tyr Ala Glu  
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Val Lys Phe Gln

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<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 260

caaagcctgc gcctggtctg tg 22

<210> 261

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 261

ttctggagcc cagagggtgc tgag 24

<210> 262

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe



<400> 262

ggagctgcca cccattcaaa tggagcacga aggagagttc acctg 45

<210> 263

<211> 2857

<212> DNA

<213> Homo sapiens

<400> 263

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caacagaaaa ctctcaaca aagaaagtca agcagccagt gcgatctcat 150

ttgagagtga agcgtggctg ggtgtggaac caatttttg taccagagga 200

aatgaatacg actagtcac acatcggcca gctaagatct gatttagaca 250

atggaaacaa ttcttccag tacaagcttt tgggagctgg agctggaagt 300

actttatca ttgatgaaag aacaggtgac atatatgcca tacagaagct 350

tgatagagag gagegatccc tctacatctt aagagcccag gtaatagaca 400

tcgctactgg aagggtgtg gaacctgagt ctgagttgt catcaaagtt 450

tcggatatca atgacaatga accaaaattc ctagatgaac cttatgaggc 500

cattgtacca gagatgtctc cagaaggaac attagttatc caggtgacag 550

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agcttacttc aaggccagcc atattttct gttgaaccaa caacaggagt 650

cataagaata tcttctaaaa tggatagaga actgcaagat gagtattggg 700

taatcattca agccaaggac atgattggtc agccaggagc gttgtctgga 750

acaacaagtg tattaattaa actttcagat gttaatgaca ataagcctat 800

atttaaagaa agtttatacc gcttgactgt ctctgaatct gcacccactg 850

ggacttctat aggaacaatc atggcatatg ataatgacat aggagagaat 900

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atttaaa 2857

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<211> 772

<212> PRT

<213> Homo sapiens

<400> 264

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Leu Trp Pro Cys Leu Gly Ala Thr Glu Asn Ser Gln Thr Lys Lys

20 25 30

Val Lys Gln Pro Val Arg Ser His Leu Arg Val Lys Arg Gly Trp  
35 40 45

Val Trp Asn Gln Phe Phe Val Pro Glu Glu Met Asn Thr Thr Ser  
50 55 60

His His Ile Gly Gln Leu Arg Ser Asp Leu Asp Asn Gly Asn Asn  
65 70 75

Ser Phe Gln Tyr Lys Leu Leu Gly Ala Gly Ala Gly Ser Thr Phe  
80 85 90

Ile Ile Asp Glu Arg Thr Gly Asp Ile Tyr Ala Ile Gln Lys Leu  
95 100 105

Asp Arg Glu Glu Arg Ser Leu Tyr Ile Leu Arg Ala Gln Val Ile  
110 115 120

Asp Ile Ala Thr Gly Arg Ala Val Glu Pro Glu Ser Glu Phe Val  
125 130 135

Ile Lys Val Ser Asp Ile Asn Asp Asn Glu Pro Lys Phe Leu Asp  
140 145 150

Glu Pro Tyr Glu Ala Ile Val Pro Glu Met Ser Pro Glu Gly Thr  
155 160 165

Leu Val Ile Gln Val Thr Ala Ser Asp Ala Asp Asp Pro Ser Ser  
170 175 180

Gly Asn Asn Ala Arg Leu Leu Tyr Ser Leu Leu Gln Gly Gln Pro  
185 190 195

Tyr Phe Ser Val Glu Pro Thr Thr Gly Val Ile Arg Ile Ser Ser  
200 205 210

Lys Met Asp Arg Glu Leu Gln Asp Glu Tyr Trp Val Ile Ile Gln  
215 220 225

Ala Lys Asp Met Ile Gly Gln Pro Gly Ala Leu Ser Gly Thr Thr  
230 235 240

Ser Val Leu Ile Lys Leu Ser Asp Val Asn Asp Asn Lys Pro Ile  
245 250 255

Phe Lys Glu Ser Leu Tyr Arg Leu Thr Val Ser Glu Ser Ala Pro  
260 265 270

Thr Gly Thr Ser Ile Gly Thr Ile Met Ala Tyr Asp Asn Asp Ile  
275 280 285

Gly Glu Asn Ala Glu Met Asp Tyr Ser Ile Glu Glu Asp Asp Ser  
290 295 300

Gln Thr Phe Asp Ile Ile Thr Asn His Glu Thr Gln Glu Gly Ile  
305 310 315

Val Ile Leu Lys Lys Lys Val Asp Phe Glu His Gln Asn His Tyr  
320 325 330

Gly Ile Arg Ala Lys Val Lys Asn His His Val Pro Glu Gln Leu  
335 340 345

Met Lys Tyr His Thr Glu Ala Ser Thr Thr Phe Ile Lys Ile Gln  
350 355 360

Val Glu Asp Val Asp Glu Pro Pro Leu Phe Leu Leu Pro Tyr Tyr  
365 370 375

Val Phe Glu Val Phe Glu Glu Thr Pro Gln Gly Ser Phe Val Gly  
380 385 390

Val Val Ser Ala Thr Asp Pro Asp Asn Arg Lys Ser Pro Ile Arg  
395 400 405

Tyr Ser Ile Thr Arg Ser Lys Val Phe Asn Ile Asn Asp Asn Gly  
410 415 420

Thr Ile Thr Thr Ser Asn Ser Leu Asp Arg Glu Ile Ser Ala Trp  
425 430 435

Tyr Asn Leu Ser Ile Thr Ala Thr Glu Lys Tyr Asn Ile Glu Gln  
440 445 450

Ile Ser Ser Ile Pro Leu Tyr Val Gln Val Leu Asn Ile Asn Asp  
455 460 465

His Ala Pro Glu Phe Ser Gln Tyr Tyr Glu Thr Tyr Val Cys Glu  
470 475 480

Asn Ala Gly Ser Gly Gln Val Ile Gln Thr Ile Ser Ala Val Asp  
485 490 495

Arg Asp Glu Ser Ile Glu Glu His His Phe Tyr Phe Asn Leu Ser  
500 505 510

Val Glu Asp Thr Asn Asn Ser Ser Phe Thr Ile Ile Asp Asn Gln  
515 520 525

Asp Asn Thr Ala Val Ile Leu Thr Asn Arg Thr Gly Phe Asn Leu  
530 535 540

Gln Glu Glu Pro Val Phe Tyr Ile Ser Ile Leu Ile Ala Asp Asn  
545 550 555

Gly Ile Pro Ser Leu Thr Ser Thr Asn Thr Leu Thr Ile His Val  
560 565 570

Cys Asp Cys Gly Asp Ser Gly Ser Thr Gln Thr Cys Gln Tyr Gln  
575 580 585

Glu Leu Val Leu Ser Met Gly Phe Lys Thr Glu Val Ile Ile Ala  
590 595 600

Ile Leu Ile Cys Ile Met Ile Ile Phe Gly Phe Ile Phe Leu Thr  
605 610 615

Leu Gly Leu Lys Gln Arg Arg Lys Gln Ile Leu Phe Pro Glu Lys  
620 625 630

Ser Glu Asp Phe Arg Glu Asn Ile Phe Gln Tyr Asp Asp Glu Gly  
635 640 645

Gly Gly Glu Glu Asp Thr Glu Ala Phe Asp Ile Ala Glu Leu Arg  
650 655 660

Ser Ser Thr Ile Met Arg Glu Arg Lys Thr Arg Lys Thr Thr Ser  
665 670 675

Ala Glu Ile Arg Ser Leu Tyr Arg Gln Ser Leu Gln Val Gly Pro  
680 685 690

Asp Ser Ala Ile Phe Arg Lys Phe Ile Leu Glu Lys Leu Glu Glu  
695 700 705

Ala Asn Thr Asp Pro Cys Ala Pro Pro Phe Asp Ser Leu Gln Thr  
710 715 720

Tyr Ala Phe Glu Gly Thr Gly Ser Leu Ala Gly Ser Leu Ser Ser  
725 730 735

Leu Glu Ser Ala Val Ser Asp Gln Asp Glu Ser Tyr Asp Tyr Leu  
740 745 750

Asn Glu Leu Gly Pro Arg Phe Lys Arg Leu Ala Cys Met Phe Gly  
755 760 765

Ser Ala Val Gln Ser Asn Asn  
770

<210> 265  
<211> 349  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 24, 60, 141, 226, 228, 249, 252  
<223> unknown base

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attcaagcca aggacatgat tggcagcca ggagcgttgt ntggaacaac 150  
  
aagtgatta attaaacttt cagatgttaa tgacaataag cctatatta 200  
  
aagaaagttt ataccgcttg actgtntntg aatctgcacc cactgggant 250  
  
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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 266

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<210> 267

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 267

aagtgggtgga agcctccagt gtgg 24

<210> 268

<211> 52

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 268

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gc 52

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<211> 2747

<212> DNA

<213> Homo sapiens

<400> 269

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cccgccctaa cttcctccgc ggggccccagc caccttcggg agtccgggtt 150

gcccacctgc aaactctccg cttctgcac ctgccacccc tgagccagcg 200

cgggcccccg agcgagtcac ggccaacgcg gggctgcagc tgttgggctt 250



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gttttggtgt tgcttttcaa atgtttgaaa ataaaaaaaa tgtaag 2747

<210> 270

<211> 211

<212> PRT

<213> Homo sapiens

<400> 270

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Leu Gly Trp Ile Gly Ala Ile Val Ser Thr Ala Leu Pro Gln Trp

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Arg Ile Tyr Ser Tyr Ala Gly Asp Asn Ile Val Thr Ala Gln Ala

35 40 45

Met Tyr Glu Gly Leu Trp Met Ser Cys Val Ser Gln Ser Thr Gly

50 55 60

Gln Ile Gln Cys Lys Val Phe Asp Ser Leu Leu Asn Leu Ser Ser

65 70 75

Thr Leu Gln Ala Thr Arg Ala Leu Met Val Val Gly Ile Leu Leu

80 85 90

Gly Val Ile Ala Ile Phe Val Ala Thr Val Gly Met Lys Cys Met

95 100 105

Lys Cys Leu Glu Asp Asp Glu Val Gln Lys Met Arg Met Ala Val

110 115 120

Ile Gly Gly Ala Ile Phe Leu Leu Ala Gly Leu Ala Ile Leu Val

125 130 135

Ala Thr Ala Trp Tyr Gly Asn Arg Ile Val Gln Glu Phe Tyr Asp

140 145 150

Pro Met Thr Pro Val Asn Ala Arg Tyr Glu Phe Gly Gln Ala Leu

155 160 165

Phe Thr Gly Trp Ala Ala Ala Ser Leu Cys Leu Leu Gly Gly Ala  
170 175 180

Leu Leu Cys Cys Ser Cys Pro Arg Lys Thr Thr Ser Tyr Pro Thr  
185 190 195

Pro Arg Pro Tyr Pro Lys Pro Ala Pro Ser Ser Gly Lys Asp Tyr  
200 205 210

Val

<210> 271

<211> 564

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 21, 69, 163, 434, 436, 444

<223> unknown base

<400> 271

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ggatggatcg gcgccatcnt cacactgccc ttccccagtg gaggatttta 100

ctccctatgc tggcgacaac atcgtgaccg cccagcccat gtacgagggg 150

ctgtggatgt ccngcgtgtc gcagagcacc gggcagatcc agtgcaaagt 200

ctttgactcc ttgtgaatc tgagcagcac attgcaagca acccgtgcct 250

tgatggtggt tggcatcctc ctgggagtga tagcaatctt tgtggccacc 300

gttggcatga agtgtatgaa gtgcttgga gacgatgagg tgcagaagat 350

gaggatggct gtcattgggg gcgcgatatt tcttcttgca ggtctggcta 400

ttttagttgc cacagcatgg tatggcaata gaancnttca acanttctat 450

gaccctatga cccagtc aa tgccaggtac gaatttggtc aggtctctt 500

cactggctgg gctgctgctt ctctctgcct tctgggaggt gccctacttt 550

gctgttcctg tccc 564

<210> 272

<211> 498

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 30, 49, 102, 141, 147, 171, 324-325, 339-341

<223> unknown base

<400> 272

acccttgacc caacgcggcc ccccgaccgn tcatggcca aacgcgggnc 50

tccagctgtt gggttcatt cccccctcc tgggatggac cggcgcccat 100

cntcagcact gccctgcccc agtggaggat ttactcctat nccggcnaca 150

acatcgtgac cgcccaggcc ntgtacgagg ggctgtggat gtcctgcgtg 200

tcgcagagca ccgggcagat ccagtgcaaa gtctttgact cccttgctga 250

atctgagcag cacattgcaa gcaaccctg ccttgatggt ggttggcatc 300

ctcctgggag tgatagcaat cttntggcc accgttgtnn ntgaagtga 350

tgaagtgctt ggaagacgat gaggtgcaga agatgaggat ggctgtcatt 400

gggggcgcga tatttcttct tgcaggtctg gctatttag ttgccacagc 450

atggtatggc aatagaatcg ttcaagaatt ctatgaccct atgaccga 498

<210> 273

<211> 552

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 25, 57, 67, 94-95, 116, 152, 165, 212, 233, 392-394

<223> unknown base

<400> 273

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gatgaancgc gccatentca gactccctgc cccatggaga tttncctat 100  
gctggcgaca acatcntgac cccagccat gtacgagggg cttgaacgt 150  
cngcgtgtcg cagancaccg ggcagatcca gtgcaaagtc ttgactcct 200  
tgctgaatct gngcagcaca ttgcagcaac cntgccctg atggtggttg 250  
gcatcctcct gggagtata gcaatctttg tggccaccgt tggcatgaag 300  
tgtatgaagt gcttggaaga cgatgagggt cagaagatga ggatggctgt 350  
cattgggggc gcgatatttc ttcttcagg tctggctatt tnnngttgcc 400  
acagcatggt atggcaatag aatcgttcaa gaattctatg accctatgac 450  
cccagtcaat gccaggtacg aatttggtca ggctctcttc actggctggg 500  
ctgctgcttc tctctgcctt ctgggaggtg ccctactttg ctgttcctgc 550  
ga 552

<210> 274

<211> 526

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 25, 50, 60, 123, 127, 370, 395, 397-398, 402-403, 405-407

<223> unknown base

<400> 274

attctccct cctggatgga tcgncacc gtcacattgc ctccccan 50  
tgaggattn actcctatgc tggcgacaac atcgtgaccc cccaggccat 100  
ttaccgaggg gctttgatg tcntgcntgt cgcagagcac cgggcagatc 150  
ccagtgaaa gtcttgact ccttgctgaa tctgagcagc acattgcaag 200  
caaccgtgc cttgatgggg ttggcatcct cctgggagtg atagcaacct 250

ttgtggccac cggtggcatg aagtgtatga agtgcttga agacgatgag 300  
gtgccagaag atgaggatgg ctgtcattgg gggcgcgata tttctgttg 350  
caggtctggc tattttagtn gccacagcat ggtatggcaa tagantnntt 400  
cnnnnntct atgaccctat gacccagtc aatgccaggt acgaatttg 450  
tcaggctctc ttcactggct gggctgctgc ttctctctgc cttctgggag 500  
gtgccctact ttgctgttcc tgtccc 526

<210> 275  
<211> 398  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 22, 61, 91, 144, 238-239, 262, 265-266, 271, 274  
<223> unknown base

<400> 275  
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gcagcacatt ncaagcaacc ccttgccctg aaggtggttg ncatccccc 100  
tgaggagtga tagcaatctt tgggccacc gttggcatga agtntatga 150  
gtgcttgga gacgatgagg tgcagaagat gaggatggct gtcattgggg 200  
gcgcgatatt tcttctgca ggtctggcta ttttagtnnc cacagcatgg 250  
tatggcaata gnatnnttcg nggnttctat gaccctatga cccagtcaa 300  
tgccaggtag gaattgggc aggtctctt cactggctgg gctgctgctt 350  
ctctctgcct tctgggagg gccctacttt gctgttctg tccccgaa 398

<210> 276  
<211> 495  
<212> DNA  
<213> Homo sapiens

<220>

<221> unsure

<222> 39, 58, 130, 234, 314, 364, 427, 450, 461, 476

<223> unknown base

<400> 276

agcaatgccc tgccccagt ggaggattaa ttctatgnt ggggacaaca 50

ttgtgacngc ccaggccatg tacggggggc tgtggatgtc ctgcgtgtcg 100

cagagcaccg ggcagatcca gtgcaaagtn ttgactcct tgctgaattt 150

gagcagcaca ttgaagcaa cccgtgcctt gatggtggtt ggcattctcc 200

tgggagtgat agcaatcttt gtggccaccg tggnaatgaa gtgtatgaag 250

tgcttgaag acgatgaggt gcagaagatg aggatggctg tcattggggg 300

cgcgatattt ctnttgcag gtctggctat ttagttgcc acagcatggt 350

atggcaatag aatngttcaa gaattttatg accctatgac cccagtcaat 400

gccaggtacg aatttggta ggcttnttc actggctggg ctgctgcttn 450

ttctgcctt ntgggaggtg ccctantttg ctgttctgc gaacc 495

<210> 277

<211> 200

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 34, 87, 138, 147, 163, 165-166, 172

<223> unknown base

<400> 277

tcataggggg gcgcgatatt tttcttgca ggtntggta ttttagtgc 50

cacagcatgg tatggcaata gaatcgtca agaattntat gaccctatga 100

ccccagtaa tgccaggtac gaatttggc aggctctntt cactggntgg 150

gctgctgctt cntnngcct tntgggaggt gccctacttt gctgttctg 200

<210> 278



<211> 542  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 26, 43, 55, 77, 198, 361-362, 391-392, 396  
<223> unknown base

<400> 278  
ttcttgggat ggtccgccc ccatctcac atgccctgcc cnttggagat 50  
  
ttacncctat gctggcgaac aacatctga ccgcccaggc catgtacgag 100  
  
gggctgtgga atgtcctgcg tgtcccagag caccgggcag atccagtga 150  
  
aagtcttga ctcttctg aatctgagca gcacattgca agcaacctg 200  
  
ccttgatggt ggttggcatc ctctgggag tgatagcaat ctttgggcc 250  
  
accgttggca tgaaagtga tgaagtgctt ggaagacgat gaggtgcaga 300  
  
agatgaggat ggctgtcatt gggggcgcga tatttcttct tgcaggtctg 350  
  
gctattttag nngccacagc atggtatggc aatcagaccc nntcanaaac 400  
  
tctatgacc tatgaccca gtcaatgcca ggtacgaatt tggtcaggct 450  
  
ctcttactg gctgggctgc tgcttctc tgccttctgg gaggtgcct 500  
  
actttgctgt tcctgtccc gaaaaacaac ctctaccca cg 542

<210> 279  
<211> 548  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 90, 115, 147, 228, 387  
<223> unknown base

<400> 279  
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ccatgctcag cactgcctg ccccatggag gatttactcn tatgctggcg 100  
acaacatcgt gaccncccag gccatgtacg aggggctgtg gatgtcngcg 150  
tgtcgcagag caccgggcag atccagtga aagtcttga ctccttgctg 200  
aatctgagca gcacattga agcaacctg ccttgatggg ggttggcatc 250  
ctcctgggag tgatagcaat ctttgggcc accgttggca tgaagtgtat 300  
gaagtgctg gaagacgat aggtgcagaa gatgaggatg gctgtcattg 350  
ggggcgcat atttcttct gcaggtctgg ctattntag ttgccacagc 400  
atggtatggc aatagaatcg ttcaagaatt ctatgacct atgacccag 450  
tcaatgccag gtacgaatt ggtcaggctc tcttactgg ctgggctgt 500  
gcttctctct gccttctggg aggtgcccta ctttgctgtt cctgcgaa 548

<210> 280

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 280

cgagcgagtc atggccaacg c 21

<210> 281

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 281

gtgtcacacg tagtctttcc cgctgg 26

<210> 282

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 282

ctgcagctgt tgggcttcat tctcgccttc ctgggatgga tcg 43

<210> 283

<211> 2285

<212> DNA

<213> Homo sapiens

<400> 283

gcgtgccgtc agctgccgg gcaccgggc ctgccctcg cctccgccc 50

ctgcgcctgc accgcgtaga ccgaccccc cctccagcgc gccacccgg 100

tagaggacc cgcgccgtgc ccgaccggt cccgccttt ttgtaaaact 150

taaagcgggc gcagcattaa cgctccgc cccggtgacc tctcagggt 200

ctcccccca aagggtgctc gccgctaagg aacatggcga aggtggagca 250

ggtctgagc ctgagccgc agcacgagct caaatccga ggtccctca 300

ccgatgttg caccaccaac ctaaagcttg gcaaccgac agaccgaaat 350

gtgtgttta aggtgaagac tacagacca cgtaggtact gtgtgaggcc 400

caacagcga atcatcgtg caggggcctc aattaatgta tctgtgatg 450

tacgccttt cgattatgat cccaatgaga aaagtaaaca caagtttatg 500

gttcagtcta tgttgctc aactgacct tcagatatgg aagcagtatg 550

gaaggaggca aaaccggaag accttatgga ttcaaaactt agatgtgtg 600

ttgaattgcc agcagagaat gataaaccac atgatgtaga aataataaa 650

attatatcca caactgcac aaagacagaa acaccaatag tgtctaagtc 700

tctgagttct tctttgatg acaccgaagt taagaaggtt atggaagaat 750

gtaagaggct gcaagtgaa gttcagaggc tacgggagga gaacaagcag 800

ttcaaggaag aagatggact gcggatgagg aagacagtgc agagcaacag 850  
ccccattca gcattagccc caactgggaa ggaagaaggc cttagcacc 900  
ggctcttggc tctgggtggt ttgttcitta tcgttggtgt aattattggg 950  
aagattgcct ttagaggta gcatgcacag gatggtaaat tggattggtg 1000  
gatccacat atcatgggat ttaaatttat cataaccatg tgtaaaaaga 1050  
aattaatga tgatgacatc tcacaggtct tgcctttaa ttaccctcc 1100  
ctgcacacac atacacagat acacacacac aatataatg taacgatctt 1150  
ttagaaagt aaaaatgtat agtaactgat tgagggggaa aaagaatgat 1200  
ctttattaat gacaaggga accatgagta atgccacaat ggcattattg 1250  
aatgtcatt ttaaacattg gtaggccttg gtacatgatg ctggattacc 1300  
tctctaaaa tgacaccctt cctcgcctgt tggctgtggc ccttggggag 1350  
ctggagccca gcatgctggg gagtgcggtc agtccacac agtagtccc 1400  
acgtggccca ctccggccc aggctgctt cctgtcttc agttctgtcc 1450  
aagccatcag ctcttggga ctgatgaaca gattcagaag cccaaaggaa 1500  
ttgactgtg gcagcatcag acgtactct cataagtga aggcgtgtgt 1550  
tgactgattg acccagcgt ttgaaataa atggcagtgc tttgttact 1600  
taaagggacc aagctaaatt tgtattggt catgtagtga agtcaaactg 1650  
ttattcagag atgttaatg catattaac ttattaatg tatttcatct 1700  
catgtttct tattgtcaca agagtacagt taatgctgcg tgctgtgaa 1750  
ctctgttggg tgaactggta ttgctgtgg agggctgtgg gctcctctgt 1800  
ctctggagag tctggcatg tggagggtgg gtttattggg atgctggaga 1850  
agagctgcca ggaagtgtt ttctgggtc agtaaataac aactgcata 1900  
gggagggaaa ttctcagtag tgacagtcaa ctctaggtta cctttttaa 1950

tgaagagtag tcagtcttct agattgttct tataccacct ctcaaccatt 2000

actcacactt ccagcgccca ggtccaagtc tgagcctgac ctccccttgg 2050

ggacctagcc tggagtcagg acaaattgat cgggctgcag agggtagaa 2100

gcgagggcac cagcagttgt ggggtggggag caagggaaga gagaaactct 2150

tcagcgaatc cttctagtag tagttgagag ttgactgtg aattaattt 2200

atgccataaa agaccaaccc agttctgttt gactatgtag catcttgaaa 2250

agaaaaatta taataaagcc ccaaaattaa gaaaa 2285

<210> 284

<211> 243

<212> PRT

<213> Homo sapiens

<400> 284

Met Ala Lys Val Glu Gln Val Leu Ser Leu Glu Pro Gln His Glu

1 5 10 15

Leu Lys Phe Arg Gly Pro Phe Thr Asp Val Val Thr Thr Asn Leu

20 25 30

Lys Leu Gly Asn Pro Thr Asp Arg Asn Val Cys Phe Lys Val Lys

35 40 45

Thr Thr Ala Pro Arg Arg Tyr Cys Val Arg Pro Asn Ser Gly Ile

50 55 60

Ile Asp Ala Gly Ala Ser Ile Asn Val Ser Val Met Leu Gln Pro

65 70 75

Phe Asp Tyr Asp Pro Asn Glu Lys Ser Lys His Lys Phe Met Val

80 85 90

Gln Ser Met Phe Ala Pro Thr Asp Thr Ser Asp Met Glu Ala Val

95 100 105

Trp Lys Glu Ala Lys Pro Glu Asp Leu Met Asp Ser Lys Leu Arg

110 115 120

Cys Val Phe Glu Leu Pro Ala Glu Asn Asp Lys Pro His Asp Val

125	130	135
Glu Ile Asn Lys Ile Ile Ser Thr Thr Ala Ser Lys Thr Glu Thr		
140	145	150
Pro Ile Val Ser Lys Ser Leu Ser Ser Ser Leu Asp Asp Thr Glu		
155	160	165
Val Lys Lys Val Met Glu Glu Cys Lys Arg Leu Gln Gly Glu Val		
170	175	180
Gln Arg Leu Arg Glu Glu Asn Lys Gln Phe Lys Glu Glu Asp Gly		
185	190	195
Leu Arg Met Arg Lys Thr Val Gln Ser Asn Ser Pro Ile Ser Ala		
200	205	210
Leu Ala Pro Thr Gly Lys Glu Glu Gly Leu Ser Thr Arg Leu Leu		
215	220	225
Ala Leu Val Val Leu Phe Phe Ile Val Gly Val Ile Ile Gly Lys		
230	235	240

Ile Ala Leu

<210> 285  
 <211> 418  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 40, 53, 68, 119, 134, 177-178, 255  
 <223> unknown base

<400> 285  
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 ctggagtcag gacaatggnt cgggctgcag aggnntagaa gcgagggcac 150  
 cagcagtttt ggggtggggag caagggnnga gagaaactct tcagcgaatc 200

cttctagtag tagttgagag ttgactgtg aattaatttt atgccataaa 250  
agacnaaccc agttctgttt gactatgtag catcttgaaa agaaaaatta 300  
taataaagcc ccaaaattaa gaattctttt gtcattttgt cacatttgct 350  
ctatgggggg aattattatt ttatcatttt tattattttg ccattggaag 400  
gttaacttta aaatgagc 418

<210> 286  
<211> 543  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 73, 97  
<223> unknown base

<400> 286  
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gattacctcc ttaatgaca ccnttcctcg cctgttggtg ctggccnttg 100  
gggagctgga gccccagcat gctggggagt gcggtcagct ccacacagta 150  
gtccccacgt ggcccactcc cggcccaggc tgctttccgt gtcttcagtt 200  
ctgtccaagc catcagctcc ttgggactga tgaacagagt cagaagccca 250  
aaggaattgc cactgtggca gcatcagacg tactcgtcat aagtgagagg 300  
cgtgtgttga ctgattgacc cagcgctttg gaaataaatg gcagtgcctt 350  
gttcacttaa agggaccaag ctaaattgta ttggttcatg tagtgaagtc 400  
aaactgttat tcagagatgt ttaatgcata ttaacttat ttaatgtatt 450  
tcatctcatg ttttcttatt gtcacaagag tacagttaat gctgcgtgct 500  
gctgaactct gttgggtgaa ctggtattgc tgctggaggg ctg 543

<210> 287  
<211> 270

<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 38, 64, 72, 164, 198, 200, 220, 222, 229, 242  
<223> unknown base

<400> 287  
ccctggtggt ttgttcttt aattcgttg tgtaattntt gggaagattg 50  
  
ctttagagg tagnatgcac cnggctggta aattggattg gtggatccac 100  
  
catatccatg ggatttaaatt tatcataac catgtgtaa aagaaattaa 150  
  
tgtatgatga catntcacag gtattgcctt taaattaccc atccctgnan 200  
  
acacatacac agatacacan anacaaatnt aatgtaacga tnttttagaa 250  
  
agttaaaaat gtatagtaac 270

<210> 288  
<211> 428  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 35, 116, 129, 197, 278, 294, 297, 349, 351  
<223> unknown base

<400> 288  
ggtggcccat tcccgGCCCA ggctgcttC cggtnntcag ttctgtccaa 50  
  
gccatcagct ccttgggact gatgaacaga gtcagaagcc caaaggaatt 100  
  
gcactgtggc agcatnagac gtacttgtna taagtgagag gcgtgtgttg 150  
  
actgattgac ccagcgcttt ggaaataaat ggcagtgcctt tgttcantta 200  
  
aagggaacaa gctaaatttg tattggttca tgtagtgaag tcaaactgtt 250  
  
attcagagat gtttaatgca tatttaantt atttaatgta tttnatntca 300  
  
tgttttctta ttgtcacaag agtacagtta atgctgcgtg ctgctgaant 350



ntgttgggtg aactggtatt gctgctggag ggctgtgggc tcctctgtct 400

ttggagagtc tggcatgtg gaggtggg 428

<210> 289

<211> 320

<212> DNA

<213> Homo sapiens

<400> 289

tgctttccgt gtcttcagtt ctgtccaagc catcagctcc ttgggacttg 50

atgaacagag tcagaagccc aaaggaattg cactgtggca gcatcagacg 100

tactcgtcat aagtgagagg cgtgtgttga ctgattgacc cagcgctttg 150

gaaataaatg gcagtgcctt gtccacttaa agggaccaag ctaaatttgt 200

attggttcat gtagtgaagt caaactgtta ttcagagatg ttaatgcat 250

atttaactta ttaatgtat ttcattctcat gttttcttat tgcacaaga 300

gtacagttaa tgctgcgtgc 320

<210> 290

<211> 609

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 57, 60, 186, 235, 244, 304, 339, 355, 359, 361, 387, 432, 441,  
447, 481, 513, 532, 584, 598

<223> unknown base

<400> 290

aaacctttaa aagttgaggg gaaaagaatg atcctttatt aatgacaagg 50

gaaacctgn gtaatgccac aatggcatat tgtaaatgtc attttaaaca 100

ttggtaggcc ttgtacatg atgctggatt acctctctta aatgacacc 150

cttcctcgcc tgttggtgct ggcccttggg gagctngagc ccagcatgct 200

ggggagtgcg gtctgtcca cacagtagtc cccangtggc ccantcccgg 250

cccaggctgc ttccgtgc ttcagttctg tccaagccat cagctccttg 300  
ggantgatga acagagtcag aagcccaaag gaattgcant gtggcagcat 350  
cagangtant ngtcataagt gagaggcgtg tgttgantga ttgaccagc 400  
gctttggaaa taaatggcag tgctttgttc anttaaaggg nccaagntaa 450  
atttgattg gttcatgtag tgaagcaaaa ntgtattca gagatgttta 500  
atgcatattt aanttattta atgtatttca tntcatgttt tcttattgtc 550  
acaagggtac agttaatgct gcgtgctgct gaantctgtt gggagaantg 600  
gtattgctg 609

<210> 291  
<211> 493  
<212> DNA  
<213> Homo sapiens

<400> 291  
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cacagtagtc cccacgtggc ccactcccgg cccaggctgc ttccgtgc 100  
ttcagttctg tccaagccat cagctccttg ggactgatga acagagtcag 150  
aagcccaaag gaattgcact gtggcagcat cagacgtact cgtcataagt 200  
gagaggcgtg tgttgactga ttgaccagc gctttggaaa taaatggcag 250  
tgctttgttc acttaaaggg accaagctaa atttgattg gttcatgtag 300  
tgaagcaaaa ctgtatttca gagatgttta atgcatattt aactatttta 350  
atgtatttca tctcatgttt tcttattgtc acaagagtac agttaatgct 400  
gcgtgctgct gaactctgtt gggagaactg gtattgctgc tggagggctg 450  
tgggctcttc tgtctctgga gagtctggtc atgtggaggt ggg 493

<210> 292  
<211> 27  
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 292

gcaccaccgt aggtacttgt gtgaggc 27

<210> 293

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 293

aaccaccaga gccagagcc ggg 23

<210> 294

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 294

cagcggaatc atcgatgcag gggcctcaat taatgtatct gtgatgttac 50

<210> 295

<211> 2530

<212> DNA

<213> Homo sapiens

<400> 295

gcgagctcgg ggtgctgtgg cccggccttg gcggggcggc ctccggctca 50

ggctggctga gaggctccca gctgcagcgt ccccgcccgc ctctcggga 100

gctctgatct cagctgacag tgcctcggg gaccaaaca gcctggcagg 150

gtctcacttt gttgccagg ctggagtcca gtgcatgat catggtttac 200

tgcagccttg acctcctggg ttcaagcgat cctgctgagt agctgggact 250

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atagagacag aaagttacaa cacagtttgt actactctga gatggatcca 2000  
ttcagctcat gccctcaatg tttatattgt gttatctgtt gggctctggga 2050  
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caatgtgtat tatttaaaaa tgggagaaat agtttgttct atgaaataaa 2200  
cctagtttag aaataggga gctgagacat ttaagatct caagttttta 2250  
tttaactaat actcaaaata tggacttttc atgtatgcat agggaagaca 2300  
cttcacaaat tatgaatgat catgtgttga aagccacatt attttatgct 2350  
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cctaataatg aataaaattt atgaatatga 2530

<210> 296  
<211> 413  
<212> PRT  
<213> Homo sapiens

<400> 296  
Met Glu Asn Met Leu Leu Trp Leu Ile Phe Phe Thr Pro Gly Trp  
1 5 10 15  
Thr Leu Ile Asp Gly Ser Glu Met Glu Trp Asp Phe Met Trp His  
20 25 30  
Leu Arg Lys Val Pro Arg Ile Val Ser Glu Arg Thr Phe His Leu  
35 40 45  
Thr Ser Pro Ala Phe Glu Ala Asp Ala Lys Met Met Val Asn Thr  
50 55 60  
Val Cys Gly Ile Glu Cys Gln Lys Glu Leu Pro Thr Pro Ser Leu  
65 70 75  
Ser Glu Leu Glu Asp Tyr Leu Ser Tyr Glu Thr Val Phe Glu Asn  
80 85 90  
Gly Thr Arg Thr Leu Thr Arg Val Lys Val Gln Asp Leu Val Leu  
95 100 105  
Glu Pro Thr Gln Asn Ile Thr Thr Lys Gly Val Ser Val Arg Arg  
110 115 120  
Lys Arg Gln Val Tyr Gly Thr Asp Ser Arg Phe Ser Ile Leu Asp  
125 130 135  
Lys Arg Phe Leu Thr Asn Phe Pro Phe Ser Thr Ala Val Lys Leu  
140 145 150  
Ser Thr Gly Cys Ser Gly Ile Leu Ile Ser Pro Gln His Val Leu  
155 160 165  
Thr Ala Ala His Cys Val His Asp Gly Lys Asp Tyr Val Lys Gly  
170 175 180  
Ser Lys Lys Leu Arg Val Gly Leu Leu Lys Met Arg Asn Lys Ser  
185 190 195

Gly Gly Lys Lys Arg Arg Gly Ser Lys Arg Ser Arg Arg Glu Ala  
200 205 210

Ser Gly Gly Asp Gln Arg Glu Gly Thr Arg Glu His Leu Gln Glu  
215 220 225

Arg Ala Lys Gly Gly Arg Arg Arg Lys Lys Ser Gly Arg Gly Gln  
230 235 240

Arg Ile Ala Glu Gly Arg Pro Ser Phe Gln Trp Thr Arg Val Lys  
245 250 255

Asn Thr His Ile Pro Lys Gly Trp Ala Arg Gly Gly Met Gly Asp  
260 265 270

Ala Thr Leu Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Arg Ala  
275 280 285

His Lys Lys Lys Tyr Met Glu Leu Gly Ile Ser Pro Thr Ile Lys  
290 295 300

Lys Met Pro Gly Gly Met Ile His Phe Ser Gly Phe Asp Asn Asp  
305 310 315

Arg Ala Asp Gln Leu Val Tyr Arg Phe Cys Ser Val Ser Asp Glu  
320 325 330

Ser Asn Asp Leu Leu Tyr Gln Tyr Cys Asp Ala Glu Ser Gly Ser  
335 340 345

Thr Gly Ser Gly Val Tyr Leu Arg Leu Lys Asp Pro Asp Lys Lys  
350 355 360

Asn Trp Lys Arg Lys Ile Ile Ala Val Tyr Ser Gly His Gln Trp  
365 370 375

Val Asp Val His Gly Val Gln Lys Asp Tyr Asn Val Ala Val Arg  
380 385 390

Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Leu Trp Ile His Gly  
395 400 405

Asn Asp Ala Asn Cys Ala Tyr Gly  
410

<210> 297  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 297  
gcatctgcag gagagagcga aggg 24

<210> 298  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 298  
catcgttccc gtgaatccag aggc 24

<210> 299  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 299  
gaaggaggc cttcctttca gtggacccgg gtcaagaata cccac 45

<210> 300  
<211> 1869  
<212> DNA  
<213> Homo sapiens

<400> 300  
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ccagtactgg atgtgacagc aggcagagga gcacttagca gcttattcag 100

tgtccgattc tgattccggc aaggatccaa gcatggaatg ctgccgtcgg 150



gcaactcctg gcacactgct cctctttctg gctttcctgc tcttgagttc 200  
caggaccgca cgctccgagg aggaccggga cggcctatgg gatgcctggg 250  
gcccatggag tgaatgctca cgcacctgcg ggggaggggc ctctactct 300  
ctgaggcgct gcctgagcag caagagctgt gaaggaagaa atatccgata 350  
cagaacatgc agtaatgtgg actgccacc agaagcaggt gatttccgag 400  
ctcagcaatg ctcagctcat aatgatgtca agcaccatgg ccagtttat 450  
gaatggcttc ctgtgtctaa tgacctgac aacctatgtt cactcaagt 500  
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gcatttcct atggaagtag acatattgc ctgtcttaa aaggtcctga 800  
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gatcctgtc cagccagtga cggatacaag cagatcatgc cttatgacct 1250  
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 ccctaagatg cccatcgcgc agccctgcaa cattttgac tggcctaaat 1450  
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 ctccctgcta taaacccaaa gagaaacttc cagtcgaggc caagtgcca 1650  
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 gtttaagaa agcagtgtct cactggtgt agcttcatg ggttctgaac 1800  
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 ttagttcaa aaaaaaaaa 1869

<210> 301

<211> 525

<212> PRT

<213> Homo sapiens

<400> 301

Met Glu Cys Cys Arg Arg Ala Thr Pro Gly Thr Leu Leu Leu Phe  
 1 5 10 15

Leu Ala Phe Leu Leu Leu Ser Ser Arg Thr Ala Arg Ser Glu Glu  
 20 25 30

Asp Arg Asp Gly Leu Trp Asp Ala Trp Gly Pro Trp Ser Glu Cys  
 35 40 45

Ser Arg Thr Cys Gly Gly Gly Ala Ser Tyr Ser Leu Arg Arg Cys  
 50 55 60

Leu Ser Ser Lys Ser Cys Glu Gly Arg Asn Ile Arg Tyr Arg Thr  
 65 70 75

Cys Ser Asn Val Asp Cys Pro Pro Glu Ala Gly Asp Phe Arg Ala  
80 85 90

Gln Gln Cys Ser Ala His Asn Asp Val Lys His His Gly Gln Phe  
95 100 105

Tyr Glu Trp Leu Pro Val Ser Asn Asp Pro Asp Asn Pro Cys Ser  
110 115 120

Leu Lys Cys Gln Ala Lys Gly Thr Thr Leu Val Val Glu Leu Ala  
125 130 135

Pro Lys Val Leu Asp Gly Thr Arg Cys Tyr Thr Glu Ser Leu Asp  
140 145 150

Met Cys Ile Ser Gly Leu Cys Gln Ile Val Gly Cys Asp His Gln  
155 160 165

Leu Gly Ser Thr Val Lys Glu Asp Asn Cys Gly Val Cys Asn Gly  
170 175 180

Asp Gly Ser Thr Cys Arg Leu Val Arg Gly Gln Tyr Lys Ser Gln  
185 190 195

Leu Ser Ala Thr Lys Ser Asp Asp Thr Val Val Ala Leu Pro Tyr  
200 205 210

Gly Ser Arg His Ile Arg Leu Val Leu Lys Gly Pro Asp His Leu  
215 220 225

Tyr Leu Glu Thr Lys Thr Leu Gln Gly Thr Lys Gly Glu Asn Ser  
230 235 240

Leu Ser Ser Thr Gly Thr Phe Leu Val Asp Asn Ser Ser Val Asp  
245 250 255

Phe Gln Lys Phe Pro Asp Lys Glu Ile Leu Arg Met Ala Gly Pro  
260 265 270

Leu Thr Ala Asp Phe Ile Val Lys Ile Arg Asn Ser Gly Ser Ala  
275 280 285

Asp Ser Thr Val Gln Phe Ile Phe Tyr Gln Pro Ile Ile His Arg  
290 295 300

Trp Arg Glu Thr Asp Phe Phe Pro Cys Ser Ala Thr Cys Gly Gly  
305 310 315

Gly Tyr Gln Leu Thr Ser Ala Glu Cys Tyr Asp Leu Arg Ser Asn  
320 325 330

Arg Val Val Ala Asp Gln Tyr Cys His Tyr Tyr Pro Glu Asn Ile  
335 340 345

Lys Pro Lys Pro Lys Leu Gln Glu Cys Asn Leu Asp Pro Cys Pro  
350 355 360

Ala Ser Asp Gly Tyr Lys Gln Ile Met Pro Tyr Asp Leu Tyr His  
365 370 375

Pro Leu Pro Arg Trp Glu Ala Thr Pro Trp Thr Ala Cys Ser Ser  
380 385 390

Ser Cys Gly Gly Gly Ile Gln Ser Arg Ala Val Ser Cys Val Glu  
395 400 405

Glu Asp Ile Gln Gly His Val Thr Ser Val Glu Glu Trp Lys Cys  
410 415 420

Met Tyr Thr Pro Lys Met Pro Ile Ala Gln Pro Cys Asn Ile Phe  
425 430 435

Asp Cys Pro Lys Trp Leu Ala Gln Glu Trp Ser Pro Cys Thr Val  
440 445 450

Thr Cys Gly Gln Gly Leu Arg Tyr Arg Val Val Leu Cys Ile Asp  
455 460 465

His Arg Gly Met His Thr Gly Gly Cys Ser Pro Lys Thr Lys Pro  
470 475 480

His Ile Lys Glu Glu Cys Ile Val Pro Thr Pro Cys Tyr Lys Pro  
485 490 495

Lys Glu Lys Leu Pro Val Glu Ala Lys Leu Pro Trp Phe Lys Gln  
500 505 510

Ala Gln Glu Leu Glu Glu Gly Ala Ala Val Ser Glu Glu Pro Ser  
515 520 525

<210> 302

<211> 1533

<212> DNA

<213> Homo sapiens

<400> 302

cggacgcgtg ggcggcggct gcggaactcc cgtggagggg ccggtgggcc 50

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ctgggcgggg cgctgtggct ggcggcccgc cggttcgtgg ggcccagggt 150

ccagcggctg cgcagaggcg gggaccccg cctcatgcac gggaagactg 200

tgctgatcac cggggcgaac agcggcctgg gccgcgccac ggccgccgag 250

ctactgcgcc tgggagcgcg ggtgatcatg ggctgccggg accgcgcgcg 300

cgccgaggag gcggcgggtc agtccgccg cgagctccgc caggccgcgg 350

agtgcggccc agagcctggc gtcagcgggg tgggcgagct catagtccgg 400

gagctggacc tcgcctcgct gcgctcgtg cgcgccttct gccaggaaat 450

gctccaggaa gaggctaggc tggatgtctt gatcaataac gcagggatct 500

tccagtcccc ttacatgaag actgaagatg ggtttgagat gcagttcgga 550

gtgaaccatc tggggcactt tctactacc aatcttctcc ttggactcct 600

caaaagtcca gctcccagca ggattgtggt agtttcttcc aaactttata 650

aatacggaga catcaatttt gatgacttga acagtgaaca aagctataat 700

aaaagctttt gttatagccg gagcaaactg gctaacattc ttttaccag 750

ggaactagcc cgccgcttag aaggcacaaa tgcaccgtc aatgtgttc 800

atcctgggtat tgtacggaca aatctgggga ggcacataca cattccactg 850

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cccaaagcta tggatgaatc tgttgcaaga aaactctggg atatcagtga 1050

agtgatgggt ggctgctaa aataggaaca aggagtaaaa gagctgttta 1100

taaaactgca tatcagttat atctgtgac aggaatgggtg tggattgaga 1150

acttggtact tgaagaaaaa gaattttgat attggaatag cctgctaaga 1200

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gaatttcagc aaagatgttt taaatatata tagtaagtat aatgaataat 1300

aagtacaatg aaaaatacaa ttatattgta aaattataac tgggcaagca 1350

tggatgacat attaatatat gtcagaatta agtgactcaa agtgctatcg 1400

agagggtttt caagtatctt tgagtttcat ggccaaagtg ttaactagtt 1450

ttactacaat gtttgggtgt tgtgtggaaa ttatctgcct ggtgtgtgca 1500

cacaagtctt acttgaata aattactgg tac 1533

<210> 303

<211> 336

<212> PRT

<213> Homo sapiens

<400> 303

Met Ala Val Ala Thr Ala Ala Ala Val Leu Ala Ala Leu Gly Gly

1 5 10 15

Ala Leu Trp Leu Ala Ala Arg Arg Phe Val Gly Pro Arg Val Gln

20 25 30

Arg Leu Arg Arg Gly Gly Asp Pro Gly Leu Met His Gly Lys Thr

35 40 45

Val Leu Ile Thr Gly Ala Asn Ser Gly Leu Gly Arg Ala Thr Ala

50 55 60

Ala Glu Leu Leu Arg Leu Gly Ala Arg Val Ile Met Gly Cys Arg

65 70 75

Asp Arg Ala Arg Ala Glu Glu Ala Ala Gly Gln Leu Arg Arg Glu

80 85 90

Leu Arg Gln Ala Ala Glu Cys Gly Pro Glu Pro Gly Val Ser Gly  
95 100 105

Val Gly Glu Leu Ile Val Arg Glu Leu Asp Leu Ala Ser Leu Arg  
110 115 120

Ser Val Arg Ala Phe Cys Gln Glu Met Leu Gln Glu Glu Pro Arg  
125 130 135

Leu Asp Val Leu Ile Asn Asn Ala Gly Ile Phe Gln Cys Pro Tyr  
140 145 150

Met Lys Thr Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His  
155 160 165

Leu Gly His Phe Leu Leu Thr Asn Leu Leu Leu Gly Leu Leu Lys  
170 175 180

Ser Ser Ala Pro Ser Arg Ile Val Val Val Ser Ser Lys Leu Tyr  
185 190 195

Lys Tyr Gly Asp Ile Asn Phe Asp Asp Leu Asn Ser Glu Gln Ser  
200 205 210

Tyr Asn Lys Ser Phe Cys Tyr Ser Arg Ser Lys Leu Ala Asn Ile  
215 220 225

Leu Phe Thr Arg Glu Leu Ala Arg Arg Leu Glu Gly Thr Asn Val  
230 235 240

Thr Val Asn Val Leu His Pro Gly Ile Val Arg Thr Asn Leu Gly  
245 250 255

Arg His Ile His Ile Pro Leu Leu Val Lys Pro Leu Phe Asn Leu  
260 265 270

Val Ser Trp Ala Phe Phe Lys Thr Pro Val Glu Gly Ala Gln Thr  
275 280 285

Ser Ile Tyr Leu Ala Ser Ser Pro Glu Val Glu Gly Val Ser Gly  
290 295 300

Arg Tyr Phe Gly Asp Cys Lys Glu Glu Glu Leu Leu Pro Lys Ala  
305 310 315

Met Asp Glu Ser Val Ala Arg Lys Leu Trp Asp Ile Ser Glu Val  
320 325 330

Met Val Gly Leu Leu Lys  
335

<210> 304

<211> 521

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 20, 34, 62, 87, 221, 229

<223> unknown base

<400> 304

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gcaagaaaat tntgggatat cagtgaagtg atggttngcc tgctaaaata 100

ggaacaagga gtaaaagagc tgtttataaa actgcatatc agttatatct 150

gtgatcagga atggtgtgga ttgagaactt gttacttgaa gaaaaagaat 200

tttgatattg gaatagcctg ntaagaggna catgtgggta ttttgagtt 250

actgaaaaat tatttttggg ataagagaat ttcagcaaag atgttttaa 300

tatatatagt aagtataatg aataataagt acaatgaaaa atacaattat 350

attgtaaaat tataactggg caagcatgga tgacatatta atattgtca 400

gaattaagtg actcaaagtg ctatcgagag gttttcaag tatctttgag 450

tttcatggcc aaagtgttaa ctagttttac tacaatgttt ggtgtttgtg 500

tggaattat ctgcctggct t 521

<210> 305

<211> 24

<212> DNA

<213> Artificial Sequence

<220>



<223> Synthetic oligonucleotide probe

<400> 305

ccaggaaatg ctccaggaag agcc 24

<210> 306

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 306

gcccatgaca ccaaattgaa gagtgg 26

<210> 307

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 307

aacgcaggga tcttccagtg cccttacatg aagactgaag atggg 45

<210> 308

<211> 1523

<212> DNA

<213> Homo sapiens

<400> 308

gagaggacga ggtgccgctg cctggagaat cctccgctgc cgtcggctcc 50

cggagcccag ccccttccta acccaacca acctagccca gtcccagccg 100

ccagcgctg tccctgtcac ggacccagc gttaccatgc atcctgccgt 150

cttcctatcc ttaccgacc tcagatgctc ccttctgctc ctgtaactt 200

gggttttac tcctgtaaca actgaaataa caagtcttgc tacagagaat 250

atagatgaaa tttaaaca tgctgatgtt gcttagtaa attttatgc 300

tgactggtgt cgtttcagtc agatgttgca tccaatttt gaggaagctt 350  
ccgatgtcat taaggaagaa ttccaaatg aaaatcaagt agtgtttgcc 400  
agagttgatt gtgatcagca ctctgacata gccagagat acaggataag 450  
caaataccca accctcaaat tgtttcgtaa tgggatgatg atgaagagag 500  
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggcaa 550  
caaaaaagt accccattca agaaattcgg gacttagcag aaatcaccac 600  
tcttgatcgc agcaaaagaa atatcattgg atatttgag caaaaggact 650  
cggacaacta tagagtttt gaacgagtag cgaatattt gcatgatgac 700  
tgtgccttc ttctgcatt tggggatgt tcaaaaccgg aaagatatag 750  
tggcgacaac ataactaca aaccaccagg gcattctgct ccgatatgg 800  
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gagagcaagc ccaagatgta gcaagcagtc cacctgagag ctcttccag 1300  
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gctttaaaaa ctgaaaaac agtttgtaag ctttcaaca gcagcatcaa 1400  
cctacgtggt ggaaatagta aacctatatt ttcataattc tatgtgtatt 1450

tttattttga ataacagaa agaaatttaa aaaaaaaaaa aaaaaaaaaa 1500

aaaaaaaaaa aaaaaaaaaa aaa 1523

<210> 309

<211> 406

<212> PRT

<213> Homo sapiens

<400> 309

Met His Pro Ala Val Phe Leu Ser Leu Pro Asp Leu Arg Cys Ser

1 5 10 15

Leu Leu Leu Leu Val Thr Trp Val Phe Thr Pro Val Thr Thr Glu

20 25 30

Ile Thr Ser Leu Ala Thr Glu Asn Ile Asp Glu Ile Leu Asn Asn

35 40 45

Ala Asp Val Ala Leu Val Asn Phe Tyr Ala Asp Trp Cys Arg Phe

50 55 60

Ser Gln Met Leu His Pro Ile Phe Glu Glu Ala Ser Asp Val Ile

65 70 75

Lys Glu Glu Phe Pro Asn Glu Asn Gln Val Val Phe Ala Arg Val

80 85 90

Asp Cys Asp Gln His Ser Asp Ile Ala Gln Arg Tyr Arg Ile Ser

95 100 105

Lys Tyr Pro Thr Leu Lys Leu Phe Arg Asn Gly Met Met Met Lys

110 115 120

Arg Glu Tyr Arg Gly Gln Arg Ser Val Lys Ala Leu Ala Asp Tyr

125 130 135

Ile Arg Gln Gln Lys Ser Asp Pro Ile Gln Glu Ile Arg Asp Leu

140 145 150

Ala Glu Ile Thr Thr Leu Asp Arg Ser Lys Arg Asn Ile Ile Gly

155 160 165

Tyr Phe Glu Gln Lys Asp Ser Asp Asn Tyr Arg Val Phe Glu Arg

170 175 180

Val Ala Asn Ile Leu His Asp Asp Cys Ala Phe Leu Ser Ala Phe  
185 190 195

Gly Asp Val Ser Lys Pro Glu Arg Tyr Ser Gly Asp Asn Ile Ile  
200 205 210

Tyr Lys Pro Pro Gly His Ser Ala Pro Asp Met Val Tyr Leu Gly  
215 220 225

Ala Met Thr Asn Phe Asp Val Thr Tyr Asn Trp Ile Gln Asp Lys  
230 235 240

Cys Val Pro Leu Val Arg Glu Ile Thr Phe Glu Asn Gly Glu Glu  
245 250 255

Leu Thr Glu Glu Gly Leu Pro Phe Leu Ile Leu Phe His Met Lys  
260 265 270

Glu Asp Thr Glu Ser Leu Glu Ile Phe Gln Asn Glu Val Ala Arg  
275 280 285

Gln Leu Ile Ser Glu Lys Gly Thr Ile Asn Phe Leu His Ala Asp  
290 295 300

Cys Asp Lys Phe Arg His Pro Leu Leu His Ile Gln Lys Thr Pro  
305 310 315

Ala Asp Cys Pro Val Ile Ala Ile Asp Ser Phe Arg His Met Tyr  
320 325 330

Val Phe Gly Asp Phe Lys Asp Val Leu Ile Pro Gly Lys Leu Lys  
335 340 345

Gln Phe Val Phe Asp Leu His Ser Gly Lys Leu His Arg Glu Phe  
350 355 360

His His Gly Pro Asp Pro Thr Asp Thr Ala Pro Gly Glu Gln Ala  
365 370 375

Gln Asp Val Ala Ser Ser Pro Pro Glu Ser Ser Phe Gln Lys Leu  
380 385 390

Ala Pro Ser Glu Tyr Arg Tyr Thr Leu Leu Arg Asp Arg Asp Glu  
395 400 405

Leu

<210> 310  
<211> 182  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 36, 48  
<223> unknown base

<400> 310  
attaaggaag aatticcaaa tgaaaatcaa gtagntttg ccagagtnga 50  
  
tttgatcag cactctgaca tagcccagag atacaggata agcaaatacc 100  
  
caaccctcaa attgttcgt aatgggatga tgatgaagag agaatacagg 150  
  
ggtcagcgat cagtgaagc attggcagat ta 182

<210> 311  
<211> 598  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 38, 59, 140, 169, 174, 183, 282-283, 294-295, 319, 396  
<223> unknown base

<400> 311  
agaggcctct ctggaagttg tcccgggtgt tcgccgngg agcccgggtc 50  
  
gagaggacna ggtgccgctg cctggagaat cctccgctgc cgtcggctcc 100  
  
cgagagccag ccccttccta acccaacca acctagccn gtcccagccg 150  
  
ccagcgctg tcctgtcnc gganccagc gtnaccatgc atcctgcctg 200  
  
cttcctatcc ttaccgacc tcagatgctc ccttctgctc ctggttaactt 250  
  
gggttttac tcctgtaaca actgaaataa cnngtcttga tacnnagaat 300

atagatgaaa ttttaacna tgctgatgtg gctttagtca atttttatgc 350

tgactgggtg cgtttcagtc agatgtggca tccaattttt gaggangctt 400

ccgatgtcat taaggaagaa ttccaaatg aaaatcaagt agtgtttggc 450

agagttgatt gtgatcagca ctctgacata gcccagagat acaggataag 500

caaataccca accctcaaat tgttcgtaa tgggatgatg atgaagagag 550

aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggc 598

<210> 312

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 312

tgagaggcct ctctggaagt tg 22

<210> 313

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 313

gtcagcgatc agtgaaagc 19

<210> 314

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 314

ccagaatgaa gtagctcggc 20

<210> 315  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 315  
ccgactcaaa atgcattgtc 20

<210> 316  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 316  
catttggcag gaattgtcc 19

<210> 317  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 317  
ggtgctatag gccaaggg 18

<210> 318  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 318  
ctgtatctct gggctatgtc agag 24

<210> 319

<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 319  
ctacatataa tggcacatgt cagcc 25

<210> 320  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 320  
cgtcttecta tccttaccg acctcagatg ctccctctg ctctg 46

<210> 321  
<211> 1333  
<212> DNA  
<213> Homo sapiens

<400> 321  
gcccacgcgt ccgatggcgt tcacgttcgc ggccttctgc tacatgctgg 50  
cgctgctgct cactgccgcg ctcatcttct tcgccatttg gcacattata 100  
gcattfgatg agctgaagac tgattacaag aatcctatag accagtgtaa 150  
taccctgaat cccctgttac tcccagagta cctcatccac gctttcttct 200  
gtgtcatgtt tctttgtgca gcagagtggc ttactggtg tctcaatatg 250  
cccctcttgg catatcatat ttggaggtat atgagtagac cagtgatgag 300  
tggccaggga ctctatgacc ctacaacat catgaatgca gatattctag 350  
catattgtca gaaggaagga tgggtgcaat tagcttttta tcttctagca 400  
ttttttact acctatatgg catgatctat gtttgggtga gctcttagaa 450



caacacacag aagaattggt ccagttaagt gcatgcaaaa agccaccaa 500

tgaagggatt ctatccagca agatcctgtc caagagtagc ctgtggaatc 550

tgatcagtta ctttaaaaaa tgactcctta tttttaaat gttccacat 600

tttgcttgt ggaaagactg tttcatatg ttatactcag ataaagattt 650

taaatggtat tacgtataaa ttaatatata atgattacct ctggtgtga 700

caggttgaa cttgcacttc ttaaggaaca gccataatcc tctgaatgat 750

gcattaatta ctgactgtcc tagtacattg gaagcttttg tttataggaa 800

cttgtagggc tcattttggt ttcatgaaa cagtatctaa ttataaatta 850

gctgtagata tcaggtgctt ctgatgaagt gaaaatgtat atctgactag 900

tgggaaactt catgggttcc ctcactgtc atgtcgatga ttatatatgg 950

atacatttac aaaaataaaa agcgggaatt ttccttcgc ttgaatatta 1000

tcctgtata ttgcatgaat gagagatttc ccatatttcc atcagagtaa 1050

taaatatact tgctttaatt ctttaagcata agtaaactg atataaaaat 1100

atatgctgaa ttacttgtga agaatgcatt taaagctatt ttaaagtgt 1150

ttttattgt aagacattac ttattaagaa attggttatt atgcttactg 1200

ttctaactcg gtggtaaagg tattcttaag aattgcagg tactacagat 1250

tttcaaaact gaatgagaga aaattgtata accatcctgc tgttccttta 1300

gtgcaataca ataaaactct gaaattaaga ctc 1333

<210> 322

<211> 144

<212> PRT

<213> Homo sapiens

<400> 322

Met Ala Phe Thr Phe Ala Ala Phe Cys Tyr Met Leu Ala Leu Leu

1

5

10

15

Leu Thr Ala Ala Leu Ile Phe Phe Ala Ile Trp His Ile Ile Ala  
20 25 30

Phe Asp Glu Leu Lys Thr Asp Tyr Lys Asn Pro Ile Asp Gln Cys  
35 40 45

Asn Thr Leu Asn Pro Leu Val Leu Pro Glu Tyr Leu Ile His Ala  
50 55 60

Phe Phe Cys Val Met Phe Leu Cys Ala Ala Glu Trp Leu Thr Leu  
65 70 75

Gly Leu Asn Met Pro Leu Leu Ala Tyr His Ile Trp Arg Tyr Met  
80 85 90

Ser Arg Pro Val Met Ser Gly Pro Gly Leu Tyr Asp Pro Thr Thr  
95 100 105

Ile Met Asn Ala Asp Ile Leu Ala Tyr Cys Gln Lys Glu Gly Trp  
110 115 120

Cys Lys Leu Ala Phe Tyr Leu Leu Ala Phe Phe Tyr Tyr Leu Tyr  
125 130 135

Gly Met Ile Tyr Val Leu Val Ser Ser  
140

<210> 323

<211> 477

<212> DNA

<213> Homo sapiens

<400> 323

attatagcat ttgatgagct gaagactgat tacaagatcc tatagaccag 50

tgtaataccc tgaatcccct tgtactccca gagtacctca tccacgcttt 100

cttctgtgtc atgtttcttt gtgcagcaga gtggcttaca ctgggtctca 150

atatgccctt ctggcatat catatttga ggtatatgag tagaccagtg 200

atgagtggcc caggactcta tgaccctaca accatcatga atgcagatat 250

tctagcatat tgtcagaagg aaggatggtg caaattagct tttatcttc 300

tagcatttt ttactaccta tatggcatga tctatgttt ggtgagcct 350

tagaacaaca cacagaagaa ttggccagt taagtgcag caaaaagcca 400

ccaaatgaag ggattctatc cagcaagatc ctgtccaaga gtagcctgtg 450

gaatctgatc agttacttta aaaaatg 477

<210> 324

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 324

tgtaaaacga cggccagta aatagacctg caattattaa tct 43

<210> 325

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 325

caggaaacag ctatgaccac ctgcacacct gcaaatccat t 41

<210> 326

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 326

gtgcagcaga gtggcttaca 20

<210> 327

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 327

actggaccaa ttcttctgtg 20

<210> 328

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 328

gatattctag catattgtca gaaggaagga tgggtcaaatt tagct 45

<210> 329

<211> 1174

<212> DNA

<213> Homo sapiens

<400> 329

cggacgcgtg ggggaaaccc ttccgagaaa acagcaacaa gctgagctgc 50

tgtgacagag gggaacaaga tggcggcgcc gaaggggagc ctctgggtga 100

ggaccaact ggggctcccg ccgtgctgc tgctgacct ggccttgcc 150

ggagggtcgg ggaccgcttc ggctgaagca ttgactcgg tcttggtga 200

tacggcgtct tgccaccggg cctgtcagtt gacctacccc ttgcacacct 250

accctaagga agaggagttg tacgcatgac agagagggtg caggctgttt 300

tcaattgtc agtttgtgga tgatgaatt gacttaaatt gaactaaatt 350

ggaatgtgaa tctgcatgta cagaagcata ttcccaattc gatgagcaat 400

atgcttgcca tcttggtgac cagaatcagc tgccattcgc tgaactgaga 450

caagaacaac ttatgtccct gatgccaaaa atgcacctac tcttcctct 500

aactctggtg aggtcattct ggagtacat gatggactcc gcacagagct 550

tcataacctc ttcattgact ttttatcttc aagccgatga cgaaaaata 600  
 gttatattcc agtctaagcc agaaatccag tacgcaccac atttgagca 650  
 ggagcctaca aatttgagag aatcatctct aagcaaaatg tcctatctgc 700  
 aaatgagaaa ttcacaagcg cacaggaatt ttcttgaaga tggagaaagt 750  
 gatggctttt taagatgcct ctctcttaac tctgggtgga tttaactac 800  
 aactcttgct ctctcggtga tggattgct ttggattgt tgtgcaactg 850  
 ttgctacagc tgtggagcag tatgttcct ctgagaagct gagtatctat 900  
 ggtgacttgg agtttatgaa tgaacaaaag ctaaacagat atccagcttc 950  
 ttctcttggt gttgttagat ctaaaactga agatcatgaa gaagcagggc 1000  
 ctctacctac aaaagtgaat ctgtctcatt ctgaaattta agcatttttc 1050  
 ttttaaaaga caagtgaat agacatctaa aattccactc ctcatagagc 1100  
 ttttaaatg gtttcattgg atataggcct taagaaatca ctataaaatg 1150  
 caaataaagt tactcaaatc tgtg 1174

<210> 330

<211> 323

<212> PRT

<213> Homo sapiens

<400> 330

Met Ala Ala Pro Lys Gly Ser Leu Trp Val Arg Thr Gln Leu Gly

1 5 10 15

Leu Pro Pro Leu Leu Leu Leu Thr Met Ala Leu Ala Gly Gly Ser

20 25 30

Gly Thr Ala Ser Ala Glu Ala Phe Asp Ser Val Leu Gly Asp Thr

35 40 45

Ala Ser Cys His Arg Ala Cys Gln Leu Thr Tyr Pro Leu His Thr

50 55 60

Tyr Pro Lys Glu Glu Glu Leu Tyr Ala Cys Gln Arg Gly Cys Arg

65	70	75
Leu Phe Ser Ile Cys Gln Phe Val Asp Asp Gly Ile Asp Leu Asn		
80	85	90
Arg Thr Lys Leu Glu Cys Glu Ser Ala Cys Thr Glu Ala Tyr Ser		
95	100	105
Gln Ser Asp Glu Gln Tyr Ala Cys His Leu Gly Cys Gln Asn Gln		
110	115	120
Leu Pro Phe Ala Glu Leu Arg Gln Glu Gln Leu Met Ser Leu Met		
125	130	135
Pro Lys Met His Leu Leu Phe Pro Leu Thr Leu Val Arg Ser Phe		
140	145	150
Trp Ser Asp Met Met Asp Ser Ala Gln Ser Phe Ile Thr Ser Ser		
155	160	165
Trp Thr Phe Tyr Leu Gln Ala Asp Asp Gly Lys Ile Val Ile Phe		
170	175	180
Gln Ser Lys Pro Glu Ile Gln Tyr Ala Pro His Leu Glu Gln Glu		
185	190	195
Pro Thr Asn Leu Arg Glu Ser Ser Leu Ser Lys Met Ser Tyr Leu		
200	205	210
Gln Met Arg Asn Ser Gln Ala His Arg Asn Phe Leu Glu Asp Gly		
215	220	225
Glu Ser Asp Gly Phe Leu Arg Cys Leu Ser Leu Asn Ser Gly Trp		
230	235	240
Ile Leu Thr Thr Thr Leu Val Leu Ser Val Met Val Leu Leu Trp		
245	250	255
Ile Cys Cys Ala Thr Val Ala Thr Ala Val Glu Gln Tyr Val Pro		
260	265	270
Ser Glu Lys Leu Ser Ile Tyr Gly Asp Leu Glu Phe Met Asn Glu		
275	280	285
Gln Lys Leu Asn Arg Tyr Pro Ala Ser Ser Leu Val Val Val Arg		

290 295 300

Ser Lys Thr Glu Asp His Glu Glu Ala Gly Pro Leu Pro Thr Lys  
305 310 315

Val Asn Leu Ala His Ser Glu Ile  
320

<210> 331  
<211> 350  
<212> DNA  
<213> Homo sapiens

<400> 331  
ttgggtgata cggcgtcttg ccaccgggcc tgcagttga cctaccctt 50  
gcacacctac cctaaggaag aggagttgta cgcattgcag agaggttgca 100  
ggctgttttc aattgtcag ttgtggatg atggaattga cttaaatcga 150  
actaaattgg aatgtgaatc tgcattgaca gaagcatatt cccaatctga 200  
tgagcaatat gcttgccatc ttggttgcca gaatcagctg ccattcgctg 250  
aactgagaca agaacaactt atgtccctga tgccaaaaat gcacctactc 300  
tttctctaa ctctggtgag gtcattctgg agtgacatga tggactccgc 350

<210> 332  
<211> 562  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 47  
<223> unknown base

<400> 332  
cacactggcc ggaatcttta gagtcctttg accttgacca agggctcngga 50  
aaacagcaac aagctgagct gctgtgacag agggacaacag atggcggcgc 100  
cgaaggagc ctttgggtga ggaccaact ggggctcccg ccgctgctgc 150

tgctgaccat ggccttgcc ggaggttcgg ggaccgcttc ggctgaagca 200

tttgactcgg tcttggtga tacggcgtct tgccaccggg cctgtcagtt 250

gacctacccc ttgcacacct accctaagga agaggagttg tacgcatgct 300

agagaggttg caggctgttt tcaattgtc agtttgtgga tgatggaatt 350

gacttaaact gaactaaatt ggaatgtgaa tctgcatgta cagaagcata 400

ttcccaatct gatgagcaat atgcttgcca tcttggtgc cagaatcagc 450

tgccattcgc tgaactgaga caagaacaac ttatgtcctt gatgccaaaa 500

atgcacctac tctttcctct aactctggtg aggtcattct ggagtgcacat 550

gatggactcc gc 562

<210> 333

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 333

acaagctgag ctgctgtgac ag 22

<210> 334

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 334

tgattctggc aaccaagatg gc 22

<210> 335

<211> 40

<212> DNA

<213> Artificial Sequence



<220>

<223> Synthetic oligonucleotide probe

<400> 335

atggccttgg ccggagggtc ggggaccgct tcggctgaag 40

<210> 336

<211> 1885

<212> DNA

<213> Homo sapiens

<400> 336

gcgaggtggc gatcgctgag aggcaggagg gccgaggcgg gcctgggagg 50

cggccccggag gtggggcgcc gctggggccg gcccgcacgg gcttcactg 100

aggcgccacg gcccgcgacc gagcgtgcgg actggcctcc caagcgtggg 150

gcgacaagct gccggagctg caatggggccg cggctgggga ttctgtttg 200

gcctcctggg cgccgtgtgg ctgctcagct cgggccacgg agaggagcag 250

cccccgaga cagcggcaca gaggtgcttc tgccaggta gtggttactt 300

ggatgattgt acctgtgatg ttgaaacat tgatagattt aataactaca 350

ggcttttccc aagactacaa aaacttctg aaagtgacta ctttaggtat 400

tacaagtaa acctgaagag gccgtgcct ttctggaatg acatcagcca 450

gtgtggaaga agggactgtg ctgtcaaacc atgtcaatct gatgaagtc 500

ctgatggaat taaatctgcg agctacaagt attctgaaga agccaataat 550

ctcattgaag aatgtgaaca agctgaacga ctgggagcag tgatgaatc 600

tctgagttag gaaacacaga aggctgttct tcagtggacc aagcatgatg 650

attcttcaga taacttctgt gaagctgatg acattcagtc ccctgaagct 700

gaatatgtag atttgcttct taatcctgag cgctacactg gttacaaggg 750

accagatgct tggaaaatat ggaatgtcat ctacgaagaa aactgtttta 800

agccacagac aattaaaga cctttaaatc ctttggttc tggtaaggg 850

acaagtgaag agaacacttt ttacagttgg ctagaaggtc tctgtgtaga 900  
 aaaaagagca ttctacagac ttatatctgg cctacatgca agcattaatg 950  
 tgcatttgag tgcaagatat cttttacaag agacctggtt agaaaagaaa 1000  
 tggggacaca acattacaga attcaacag cgatttgatg gaattttgac 1050  
 tgaaggagaa ggtccaagaa ggcttaagaa ctgtatttt ctctacttaa 1100  
 tagaactaag ggctttatcc aaagtgttac cattcttga gcgcccagat 1150  
 ttcaactct ttactggaaa taaaattcag gatgaggaaa acaaaatgtt 1200  
 acttctggaa atacttcatt aaatcaagtc attcctttg cattttgatg 1250  
 agaattcatt ttttctggg gataaaaaag aagcacacaa actaaaggag 1300  
 gactttcgac tgcattttag aaatattca agaattatgg attgtgttg 1350  
 ttgttttaa tgcgtctgt ggggaaagct tcagactcag ggtttgggca 1400  
 ctgctctgaa gatcttattt tctgagaaat tgatagcaaa tatgccagaa 1450  
 agtggaccta gttatgaatt ccatctaacc agacaagaaa tagtattcatt 1500  
 attcaacgca ttggaagaa ttctacaag tgtgaaagaa ttagaaaact 1550  
 tcaggaactt gttacagaat attcattaaa gaaaacaagc tgatatgtgc 1600  
 ctgtttctgg acaatggagg cgaaagagtg gaatttcatt caaaggcata 1650  
 atagcaatga cagtcttaag ccaaacttt tatataaagt tgcttttga 1700  
 aaggagaatt atattgtttt aagtaaacac atttttaaaa attgtgttaa 1750  
 gtctatgtat aatactactg tgagtaaaag taatacttta ataattgtgt 1800  
 acaaatTTTA aagTTtaata ttgaataaaa ggaggattat caaattaaaa 1850  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 1885

<210> 337

<211> 468

<212> PRT

<213> Homo sapiens

<400> 337

Met Gly Arg Gly Trp Gly Phe Leu Phe Gly Leu Leu Gly Ala Val  
1 5 10 15

Trp Leu Leu Ser Ser Gly His Gly Glu Glu Gln Pro Pro Glu Thr  
20 25 30

Ala Ala Gln Arg Cys Phe Cys Gln Val Ser Gly Tyr Leu Asp Asp  
35 40 45

Cys Thr Cys Asp Val Glu Thr Ile Asp Arg Phe Asn Asn Tyr Arg  
50 55 60

Leu Phe Pro Arg Leu Gln Lys Leu Leu Glu Ser Asp Tyr Phe Arg  
65 70 75

Tyr Tyr Lys Val Asn Leu Lys Arg Pro Cys Pro Phe Trp Asn Asp  
80 85 90

Ile Ser Gln Cys Gly Arg Arg Asp Cys Ala Val Lys Pro Cys Gln  
95 100 105

Ser Asp Glu Val Pro Asp Gly Ile Lys Ser Ala Ser Tyr Lys Tyr  
110 115 120

Ser Glu Glu Ala Asn Asn Leu Ile Glu Glu Cys Glu Gln Ala Glu  
125 130 135

Arg Leu Gly Ala Val Asp Glu Ser Leu Ser Glu Glu Thr Gln Lys  
140 145 150

Ala Val Leu Gln Trp Thr Lys His Asp Asp Ser Ser Asp Asn Phe  
155 160 165

Cys Glu Ala Asp Asp Ile Gln Ser Pro Glu Ala Glu Tyr Val Asp  
170 175 180

Leu Leu Leu Asn Pro Glu Arg Tyr Thr Gly Tyr Lys Gly Pro Asp  
185 190 195

Ala Trp Lys Ile Trp Asn Val Ile Tyr Glu Glu Asn Cys Phe Lys  
200 205 210

Pro Gln Thr Ile Lys Arg Pro Leu Asn Pro Leu Ala Ser Gly Gln  
215 220 225

Gly Thr Ser Glu Glu Asn Thr Phe Tyr Ser Trp Leu Glu Gly Leu  
230 235 240

Cys Val Glu Lys Arg Ala Phe Tyr Arg Leu Ile Ser Gly Leu His  
245 250 255

Ala Ser Ile Asn Val His Leu Ser Ala Arg Tyr Leu Leu Gln Glu  
260 265 270

Thr Trp Leu Glu Lys Lys Trp Gly His Asn Ile Thr Glu Phe Gln  
275 280 285

Gln Arg Phe Asp Gly Ile Leu Thr Glu Gly Glu Gly Pro Arg Arg  
290 295 300

Leu Lys Asn Leu Tyr Phe Leu Tyr Leu Ile Glu Leu Arg Ala Leu  
305 310 315

Ser Lys Val Leu Pro Phe Phe Glu Arg Pro Asp Phe Gln Leu Phe  
320 325 330

Thr Gly Asn Lys Ile Gln Asp Glu Glu Asn Lys Met Leu Leu Leu  
335 340 345

Glu Ile Leu His Glu Ile Lys Ser Phe Pro Leu His Phe Asp Glu  
350 355 360

Asn Ser Phe Phe Ala Gly Asp Lys Lys Glu Ala His Lys Leu Lys  
365 370 375

Glu Asp Phe Arg Leu His Phe Arg Asn Ile Ser Arg Ile Met Asp  
380 385 390

Cys Val Gly Cys Phe Lys Cys Arg Leu Trp Gly Lys Leu Gln Thr  
395 400 405

Gln Gly Leu Gly Thr Ala Leu Lys Ile Leu Phe Ser Glu Lys Leu  
410 415 420

Ile Ala Asn Met Pro Glu Ser Gly Pro Ser Tyr Glu Phe His Leu  
425 430 435

Thr Arg Gln Glu Ile Val Ser Leu Phe Asn Ala Phe Gly Arg Ile  
440 445 450

Ser Thr Ser Val Lys Glu Leu Glu Asn Phe Arg Asn Leu Leu Gln  
455 460 465

Asn Ile His

<210> 338  
<211> 507  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 101, 263, 376, 397, 426  
<223> unknown base

<400> 338  
gctggaaata tggatgtcat ctacgagaaa ctgtttaag ccacagacaa 50  
ttaaagacc tttaaatcct ttggttctg gtcaagggac aagtgaagag 100  
nacactttt acagttggct agaaggtctc tgttagaaa aaagagcatt 150  
ctacagactt atatctggcc tacatgcaag cattaatgtg catttgagtg 200  
caagatatct ttacaagag acctggttag aaaagaaatg gggacacaac 250  
attacagaat ttnaacagcg atttgatgga atttgactg aaggagaagg 300  
tccaagaagg ctaagaact tgtattttct ctacttaata gaactaaggg 350  
ctttatcaa agtggtacca ttctngagc gcccagattt tcaactnttt 400  
actggaaata aaattcagga tgaggnaaac aaaatgttac ttttgaaat 450  
acttcatgaa atcaagtcac ttccttgca tttgatgag aattcattt 500  
tttgctg 507

<210> 339  
<211> 20  
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 339

aagctgccgg agctgcaatg 20

<210> 340

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 340

ttgcttctta atcctgagcg c 21

<210> 341

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 341

aaaggaggac ttctgactgc 20

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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 345

<211> 1486

<212> DNA

<213> Homo sapiens

<400> 345

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gatgggaggg aaagtgaaga aaacagaaaa ggagagggac agaggccaga 100

ggacttctca tactggacag aaaccgatca ggcatggaac tcccccttct 150

cactcacctg ttcttgcctt tgggtgtcct gacaggtctc tgctccccct 200

ttaacctgga tgaacatcac ccacgcctat tcccagggcc accagaagct 250

gaatttgat acagtgtctt acaacatgtt gggggtggac agcgatggat 300

gctggtgggc gccccctggg atgggccttc aggcgaccgg aggggggacg 350

tttatcgctg ccctgtaggg ggggcccaca atgccccatg tgccaagggc 400

cacttaggtg actaccaact gggaaattca tctcatcctg ctgtgaatat 450

gcacctgggg atgtctctgt tagagacaga tggatgagg ggattcatgg 500

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agaaagacc cactctctaaa taaatgtttt aaaaat 1486

<210> 346

<211> 124

<212> PRT

<213> Homo sapiens

<400> 346

Met Glu Leu Pro Phe Val Thr His Leu Phe Leu Pro Leu Val Phe



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Arg Leu Phe Pro Gly Pro Pro Glu Ala Glu Phe Gly Tyr Ser Val			
35	40	45	
Leu Gln His Val Gly Gly Gly Gln Arg Trp Met Leu Val Gly Ala			
50	55	60	
Pro Trp Asp Gly Pro Ser Gly Asp Arg Arg Gly Asp Val Tyr Arg			
65	70	75	
Cys Pro Val Gly Gly Ala His Asn Ala Pro Cys Ala Lys Gly His			
80	85	90	
Leu Gly Asp Tyr Gln Leu Gly Asn Ser Ser His Pro Ala Val Asn			
95	100	105	
Met His Leu Gly Met Ser Leu Leu Glu Thr Asp Gly Asp Gly Gly			
110	115	120	
Phe Met Val Ser			

<210> 347  
 <211> 509  
 <212> DNA  
 <213> Homo sapiens

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 <222> 22  
 <223> unknown base

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 ggcatggaac tcccctcgt cactcacctg ttctgcccc tgggttcct 200

gacaggtctc tgcctccctt ttaacctgga tgaacatcac ccacgcctat 250

tcccagggcc accagaagct gaatttgat acagtgtctt acaacatgtt 300

gggggtggac agcgatggat gctggtgggc gcccctggg atgggccttc 350

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tggtgatgg 509

<210> 348

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 348

agggacagag gccagaggac ttc 23

<210> 349

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 349

caggtgcata ttcacagcag gatg 24

<210> 350

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 350

ggaactcccc ttctcactc acctgttctt gcccttggtg ttct 45

<210> 351

<211> 2056

<212> DNA

<213> Homo sapiens

<400> 351

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gcttctggg ccggctctag aacaattcag gcttcgctgc gactcagacc 150

tcagctccaa catatgcatt ctgaagaaag atggctgaga tggacagaat 200

gctttatctt ggaaagaaac aatgttctag gtcaaactga gtctaccaa 250

tgcagacttt cacaatggtt ctagaagaaa tctggacaag tctttcatg 300

tggttttct acgcattgat tccatgtttg ctcacagatg aagtggccat 350

tctgcctgcc cctcagaacc tctctgtact ctcaaccaac atgaagcatc 400

tcttgatgtg gagcccagtg atcgcgcctg gagaaacagt gtactattct 450

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<210> 352

<211> 311

<212> PRT

<213> Homo sapiens

<400> 352

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Phe Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr Asp

20 25 30

Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser

35 40 45

Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro

50 55 60

Gly Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu

65 70 75

Ser Leu Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser

80 85 90

Leu Thr Glu Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala

95 100 105

Thr Val Pro Tyr Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln

110 115 120

Thr Ser Ala Trp Ser Ile Leu Lys His Pro Phe Asn Arg Asn Ser

125 130 135

Thr Ile Leu Thr Arg Pro Gly Met Glu Ile Thr Lys Asp Gly Phe

140 145 150

His Leu Val Ile Glu Leu Glu Asp Leu Gly Pro Gln Phe Glu Phe

155 160 165

Leu Val Ala Tyr Trp Arg Arg Glu Pro Gly Ala Glu Glu His Val

170 175 180

Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu Glu Thr Met

185 190 195

Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe Val Lys  
200 205 210

Ala Ile Gly Arg Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val Glu  
215 220 225

Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe  
230 235 240

Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe Val Trp  
245 250 255

Lys Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val Val  
260 265 270

Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile  
275 280 285

Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met  
290 295 300

Ser Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser  
305 310

<210> 353  
<211> 864  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 654, 711, 748, 827  
<223> unknown base

<400> 353  
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ggcgctgggt tgat 864

<210> 354

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 354

aggcttcgct gcgactagac ctc 23

<210> 355

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 355

ccaggtcggg taaggatggt tgag 24

<210> 356

<211> 50

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 357

<211> 1670

<212> DNA

<213> Homo sapiens

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agaggcagga gctggaaagg agagagggag gaggaggagg agatgcggga 200

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gctgagagga gtaggaagat caggagctag agggagactg gagggttccg 350

ggaaaagagc agaggaaaga ggaaagacac agagagacgg gagagagaag 400

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<211> 328  
<212> PRT

<213> Homo sapiens

<400> 358

Met Gly Ala Ala Ala Arg Leu Ser Ala Pro Arg Ala Leu Val Leu  
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Trp Ala Ala Leu Gly Ala Ala Ala His Ile Gly Pro Ala Pro Asp  
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Pro Glu Asp Trp Trp Ser Tyr Lys Asp Asn Leu Gln Gly Asn Phe  
35 40 45

Val Pro Gly Pro Pro Phe Trp Gly Leu Val Asn Ala Ala Trp Ser  
50 55 60

Leu Cys Ala Val Gly Lys Arg Gln Ser Pro Val Asp Val Glu Leu  
65 70 75

Lys Arg Val Leu Tyr Asp Pro Phe Leu Pro Pro Leu Arg Leu Ser  
80 85 90

Thr Gly Gly Glu Lys Leu Arg Gly Thr Leu Tyr Asn Thr Gly Arg  
95 100 105

His Val Ser Phe Leu Pro Ala Pro Arg Pro Val Val Asn Val Ser  
110 115 120

Gly Gly Pro Leu Leu Tyr Ser His Arg Leu Ser Glu Leu Arg Leu  
125 130 135

Leu Phe Gly Ala Arg Asp Gly Ala Gly Ser Glu His Gln Ile Asn  
140 145 150

His Gln Gly Phe Ser Ala Glu Val Gln Leu Ile His Phe Asn Gln  
155 160 165

Glu Leu Tyr Gly Asn Phe Ser Ala Ala Ser Arg Gly Pro Asn Gly  
170 175 180

Leu Ala Ile Leu Ser Leu Phe Val Asn Val Ala Ser Thr Ser Asn  
185 190 195

Pro Phe Leu Ser Arg Leu Leu Asn Arg Asp Thr Ile Thr Arg Ile  
200 205 210

Ser Tyr Lys Asn Asp Ala Tyr Phe Leu Gln Asp Leu Ser Leu Glu  
215 220 225

Leu Leu Phe Pro Glu Ser Phe Gly Phe Ile Thr Tyr Gln Gly Ser  
230 235 240

Leu Ser Thr Pro Pro Cys Ser Glu Thr Val Thr Trp Ile Leu Ile  
245 250 255

Asp Arg Ala Leu Asn Ile Thr Ser Leu Gln Met His Ser Leu Arg  
260 265 270

Leu Leu Ser Gln Asn Pro Pro Ser Gln Ile Phe Gln Ser Leu Ser  
275 280 285

Gly Asn Ser Arg Pro Leu Gln Pro Leu Ala His Arg Ala Leu Arg  
290 295 300

Gly Asn Arg Asp Pro Arg His Pro Glu Arg Arg Cys Arg Gly Pro  
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Asn Tyr Arg Leu His Val Asp Gly Val Pro His Gly Arg  
320 325

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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 360

<211> 24

<212> DNA

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<223> Synthetic oligonucleotide probe

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agtaaagtga gggtaagca tggacagcca gagctttcta tgtactgtta 2700  
aaattgaggt cacatatttt cttttgtatc ctggcaaata ctctgcagg 2750  
ccaggaagta taatagcaaa aagttgaaca aagatgaact aatgtattac 2800  
attaccattg ccactgattt ttttaaatg gtaaatgacc ttgtatataa 2850  
atattgccat atcatggtac ctataatggt gatataattg tttctatgaa 2900  
aaatgtattg tgctttgata ctaaaaatct gtaaatggtt agttttggta 2950  
atttttttc tgctggtgga ttacatatt aaatttttc tgctggtgga 3000

taaacattaa aattaatcat gtttcaaaaa aaaaaaaaa 3038

<210> 363

<211> 500

<212> PRT

<213> Homo sapiens

<400> 363

Met Lys Cys Thr Ala Arg Glu Trp Leu Arg Val Thr Thr Val Leu  
1 5 10 15

Phe Met Ala Arg Ala Ile Pro Ala Met Val Val Pro Asn Ala Thr  
20 25 30

Leu Leu Glu Lys Leu Leu Glu Lys Tyr Met Asp Glu Asp Gly Glu  
35 40 45

Trp Trp Ile Ala Lys Gln Arg Gly Lys Arg Ala Ile Thr Asp Asn  
50 55 60

Asp Met Gln Ser Ile Leu Asp Leu His Asn Lys Leu Arg Ser Gln  
65 70 75

Val Tyr Pro Thr Ala Ser Asn Met Glu Tyr Met Thr Trp Asp Val  
80 85 90

Glu Leu Glu Arg Ser Ala Glu Ser Trp Ala Glu Ser Cys Leu Trp  
95 100 105

Glu His Gly Pro Ala Ser Leu Leu Pro Ser Ile Gly Gln Asn Leu  
110 115 120

Gly Ala His Trp Gly Arg Tyr Arg Pro Pro Thr Phe His Val Gln  
125 130 135

Ser Trp Tyr Asp Glu Val Lys Asp Phe Ser Tyr Pro Tyr Glu His  
140 145 150

Glu Cys Asn Pro Tyr Cys Pro Phe Arg Cys Ser Gly Pro Val Cys  
155 160 165

Thr His Tyr Thr Gln Val Val Trp Ala Thr Ser Asn Arg Ile Gly  
170 175 180

Cys Ala Ile Asn Leu Cys His Asn Met Asn Ile Trp Gly Gln Ile

185	190	195
Trp Pro Lys Ala Val Tyr Leu Val Cys Asn Tyr Ser Pro Lys Gly		
200	205	210
Asn Trp Trp Gly His Ala Pro Tyr Lys His Gly Arg Pro Cys Ser		
215	220	225
Ala Cys Pro Pro Ser Phe Gly Gly Gly Cys Arg Glu Asn Leu Cys		
230	235	240
Tyr Lys Glu Gly Ser Asp Arg Tyr Tyr Pro Pro Arg Glu Glu Glu		
245	250	255
Thr Asn Glu Ile Glu Arg Gln Gln Ser Gln Val His Asp Thr His		
260	265	270
Val Arg Thr Arg Ser Asp Asp Ser Ser Arg Asn Glu Val Ile Ser		
275	280	285
Ala Gln Gln Met Ser Gln Ile Val Ser Cys Glu Val Arg Leu Arg		
290	295	300
Asp Gln Cys Lys Gly Thr Thr Cys Asn Arg Tyr Glu Cys Pro Ala		
305	310	315
Gly Cys Leu Asp Ser Lys Ala Lys Val Ile Gly Ser Val His Tyr		
320	325	330
Glu Met Gln Ser Ser Ile Cys Arg Ala Ala Ile His Tyr Gly Ile		
335	340	345
Ile Asp Asn Asp Gly Gly Trp Val Asp Ile Thr Arg Gln Gly Arg		
350	355	360
Lys His Tyr Phe Ile Lys Ser Asn Arg Asn Gly Ile Gln Thr Ile		
365	370	375
Gly Lys Tyr Gln Ser Ala Asn Ser Phe Thr Val Ser Lys Val Thr		
380	385	390
Val Gln Ala Val Thr Cys Glu Thr Thr Val Glu Gln Leu Cys Pro		
395	400	405
Phe His Lys Pro Ala Ser His Cys Pro Arg Val Tyr Cys Pro Arg		



410 415 420

Asn Cys Met Gln Ala Asn Pro His Tyr Ala Arg Val Ile Gly Thr  
425 430 435

Arg Val Tyr Ser Asp Leu Ser Ser Ile Cys Arg Ala Ala Val His  
440 445 450

Ala Gly Val Val Arg Asn His Gly Gly Tyr Val Asp Val Met Pro  
455 460 465

Val Asp Lys Arg Lys Thr Tyr Ile Ala Ser Phe Gln Asn Gly Ile  
470 475 480

Phe Ser Glu Ser Leu Gln Asn Pro Pro Gly Gly Lys Ala Phe Arg  
485 490 495

Val Phe Ala Val Val  
500

<210> 364

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 364

ggacagaatt tgggagcaca ctgg 24

<210> 365

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 365

ccaagagtat actgtcctcg 20

<210> 366

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 366

agcacagatt ttctctacag ccccc 25

<210> 367

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 367

aaccactcca gcatgtactg ctgc 24

<210> 368

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 368

ccattcaggt gttctggccc tgtatgtaca cattatacac aggtcgtgtg 50

<210> 369

<211> 1685

<212> DNA

<213> Homo sapiens

<400> 369

gcggagacaa ggcgagagcg cagcgacagg ccacagacag ccctgggcat 50

ccaccgacgg cgcagccgga gccagcagag ccggaaggcg cgccccgggc 100

agagaaagcc gagcagagct gggtagcgct tccgggccgc cgctccgacg 150

ggccagcgcc ctccccatgt ccctgctccc acgccgcccc cctccgggtca 200

gcatgaggct cctggcggcc gcgtgctcc tgctgctgt ggcgctgtac 250

accgcgcgtg tggacgggtc caaatgcaag tgctcccga agggacccaa 300  
gatccgctac agcgacgtga agaagctgga aatgaagcca aagtaccgc 350  
actgcgagga gaagatggtt atcatcacca ccaagagcgt gtccaggtac 400  
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 aatgttaaac agtgcagtcc tctttcgaaa gctaagatga ccatgcgccc 1500  
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 cagtatatgc cgcattgtac tgctgtgtta tatgctatgt acatgtcaga 1600  
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 ataaaatata tttgaaatgt aaaaaaaaaa aaaaa 1685

<210> 370  
 <211> 111  
 <212> PRT  
 <213> Homo sapiens

<400> 370  
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 1 5 10 15  
 Leu Ala Ala Ala Leu Leu Leu Leu Leu Ala Leu Tyr Thr Ala  
 20 25 30  
 Arg Val Asp Gly Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro Lys  
 35 40 45  
 Ile Arg Tyr Ser Asp Val Lys Lys Leu Glu Met Lys Pro Lys Tyr  
 50 55 60  
 Pro His Cys Glu Glu Lys Met Val Ile Ile Thr Thr Lys Ser Val  
 65 70 75  
 Ser Arg Tyr Arg Gly Gln Glu His Cys Leu His Pro Lys Leu Gln  
 80 85 90  
 Ser Thr Lys Arg Phe Ile Lys Trp Tyr Asn Ala Trp Asn Glu Lys  
 95 100 105  
 Arg Arg Val Tyr Glu Glu  
 110

<210> 371  
 <211> 22  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 371

cagegccctc cccatgtccc tg 22

<210> 372

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 372

tcccaactgg ttggagttt tccc 24

<210> 373

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 373

ctccggtcg catgaggctc ctggcggccg ctgctctgc tgcg 45

<210> 374

<211> 3113

<212> DNA

<213> Homo sapiens

<400> 374

gccccaggga ctgctatggc ttctttgtt gttaccccc gtctgcgtca 50

tgtaaactc caatgtcctc ctgtggttaa ctgctctgc catcaagtc 100

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caaaatccgg ggcctaagaa caccgttacc caatgagatc ttgggtccag 200

tggagcagta cttaggggtc ccctatgcct cccccccac tggagagagg 250

cggtttcagc cccagaacc cccgtcctcc tggactggca tccgaaatac 300  
tactcagttt gctgctgtgt gccccagca cctggatgag agatccttac 350  
tgcattgacat gctgcccac tggtttaccg ccaatttga tactttgatg 400  
acctatgttc aagatcaaaa tgaagactgc ctttacttaa acatctacgt 450  
gcccacggaa gatggagcca acacaaagaa aaacgcagat gatataacga 500  
gtaatgaccg tgggaagac gaagatattc atgacagaa cagtaagaag 550  
cccgatcagg tctatatcca tgggggatct tacatggagg gcaccggcaa 600  
catgattgac ggcagcattt tggcaagcta cggaaacgtc atcgtgatca 650  
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gcagcaaaag gcaactatgg gctcctggat cagattcaag cactgcggtg 750  
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tctttggctc gggggctggg gcctcctgtg tcagcctgtt gaccctgtcc 850  
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aacgaaagtg gctttctggt tggaactcgt tcttcatttg cacaactga 1850

acgagatatt ccagtatgtt tcaacaacca caaaggttcc tccaccagac 1900

atgacatcat ttccctatgg caccgggcca tctcccgcca agatatggcc 1950

aaccacaaaa cgcccagcaa tcaactctgc caacaatccc aaactctta 2000

aggacctca caaacaggg cctgaggaca caactgtcct cattgaaacc 2050

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ctttgcccta ttcccttcc tatccctctg ccctaccgc tcagcaacat 2550

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agaccaggaa tgttttgtc ccactgactt aagacaaaaa tgcaaaaagg 2650

cagtcatccc atcccggcag acccttatcg ttggtgtttt ccagtattac 2700

aagatcaact tctgacctg tgaaatgta gaagtacaca ttctgttaa 2750

aataactgct ttaagatctc taccactcca atcaatgttt agtgtgatag 2800

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gaagtttaaa catttcttc tgtccacac aatggatggc tctccttaag 2950

tgaagaaaga gtcaatgaga tttgcccag cacatggagc tgtaatccag 3000

agagaaggaa acgtagaaat ttattattaa aagaatggac tgtgcagcga 3050

aatctgtacg gtctgtgca aagaggtgtt ttgccagcct gaactatatt 3100

taagagactt tgt 3113

<210> 375

<211> 816

<212> PRT

<213> Homo sapiens

<400> 375

Met Leu Asn Ser Asn Val Leu Leu Trp Leu Thr Ala Leu Ala Ile

1 5 10 15

Lys Phe Thr Leu Ile Asp Ser Gln Ala Gln Tyr Pro Val Val Asn

20 25 30

Thr Asn Tyr Gly Lys Ile Arg Gly Leu Arg Thr Pro Leu Pro Asn

35 40 45

Glu Ile Leu Gly Pro Val Glu Gln Tyr Leu Gly Val Pro Tyr Ala

50 55 60

Ser Pro Pro Thr Gly Glu Arg Arg Phe Gln Pro Pro Glu Pro Pro

65 70 75



Ser Ser Trp Thr Gly Ile Arg Asn Thr Thr Gln Phe Ala Ala Val  
80 85 90

Cys Pro Gln His Leu Asp Glu Arg Ser Leu Leu His Asp Met Leu  
95 100 105

Pro Ile Trp Phe Thr Ala Asn Leu Asp Thr Leu Met Thr Tyr Val  
110 115 120

Gln Asp Gln Asn Glu Asp Cys Leu Tyr Leu Asn Ile Tyr Val Pro  
125 130 135

Thr Glu Asp Gly Ala Asn Thr Lys Lys Asn Ala Asp Asp Ile Thr  
140 145 150

Ser Asn Asp Arg Gly Glu Asp Glu Asp Ile His Asp Gln Asn Ser  
155 160 165

Lys Lys Pro Val Met Val Tyr Ile His Gly Gly Ser Tyr Met Glu  
170 175 180

Gly Thr Gly Asn Met Ile Asp Gly Ser Ile Leu Ala Ser Tyr Gly  
185 190 195

Asn Val Ile Val Ile Thr Ile Asn Tyr Arg Leu Gly Ile Leu Gly  
200 205 210

Phe Leu Ser Thr Gly Asp Gln Ala Ala Lys Gly Asn Tyr Gly Leu  
215 220 225

Leu Asp Gln Ile Gln Ala Leu Arg Trp Ile Glu Glu Asn Val Gly  
230 235 240

Ala Phe Gly Gly Asp Pro Lys Arg Val Thr Ile Phe Gly Ser Gly  
245 250 255

Ala Gly Ala Ser Cys Val Ser Leu Leu Thr Leu Ser His Tyr Ser  
260 265 270

Glu Gly Leu Phe Gln Lys Ala Ile Ile Gln Ser Gly Thr Ala Leu  
275 280 285

Ser Ser Trp Ala Val Asn Tyr Gln Pro Ala Lys Tyr Thr Arg Ile  
290 295 300

Leu Ala Asp Lys Val Gly Cys Asn Met Leu Asp Thr Thr Asp Met  
305 310 315

Val Glu Cys Leu Arg Asn Lys Asn Tyr Lys Glu Leu Ile Gln Gln  
320 325 330

Thr Ile Thr Pro Ala Thr Tyr His Ile Ala Phe Gly Pro Val Ile  
335 340 345

Asp Gly Asp Val Ile Pro Asp Asp Pro Gln Ile Leu Met Glu Gln  
350 355 360

Gly Glu Phe Leu Asn Tyr Asp Ile Met Leu Gly Val Asn Gln Gly  
365 370 375

Glu Gly Leu Lys Phe Val Asp Gly Ile Val Asp Asn Glu Asp Gly  
380 385 390

Val Thr Pro Asn Asp Phe Asp Phe Ser Val Ser Asn Phe Val Asp  
395 400 405

Asn Leu Tyr Gly Tyr Pro Glu Gly Lys Asp Thr Leu Arg Glu Thr  
410 415 420

Ile Lys Phe Met Tyr Thr Asp Trp Ala Asp Lys Glu Asn Pro Glu  
425 430 435

Thr Arg Arg Lys Thr Leu Val Ala Leu Phe Thr Asp His Gln Trp  
440 445 450

Val Ala Pro Ala Val Ala Ala Asp Leu His Ala Gln Tyr Gly Ser  
455 460 465

Pro Thr Tyr Phe Tyr Ala Phe Tyr His His Cys Gln Ser Glu Met  
470 475 480

Lys Pro Ser Trp Ala Asp Ser Ala His Gly Asp Glu Val Pro Tyr  
485 490 495

Val Phe Gly Ile Pro Met Ile Gly Pro Thr Glu Leu Phe Ser Cys  
500 505 510

Asn Phe Ser Lys Asn Asp Val Met Leu Ser Ala Val Val Met Thr  
515 520 525

Tyr Trp Thr Asn Phe Ala Lys Thr Gly Asp Pro Asn Gln Pro Val  
530 535 540

Pro Gln Asp Thr Lys Phe Ile His Thr Lys Pro Asn Arg Phe Glu  
545 550 555

Glu Val Ala Trp Ser Lys Tyr Asn Pro Lys Asp Gln Leu Tyr Leu  
560 565 570

His Ile Gly Leu Lys Pro Arg Val Arg Asp His Tyr Arg Ala Thr  
575 580 585

Lys Val Ala Phe Trp Leu Glu Leu Val Pro His Leu His Asn Leu  
590 595 600

Asn Glu Ile Phe Gln Tyr Val Ser Thr Thr Thr Lys Val Pro Pro  
605 610 615

Pro Asp Met Thr Ser Phe Pro Tyr Gly Thr Arg Arg Ser Pro Ala  
620 625 630

Lys Ile Trp Pro Thr Thr Lys Arg Pro Ala Ile Thr Pro Ala Asn  
635 640 645

Asn Pro Lys His Ser Lys Asp Pro His Lys Thr Gly Pro Glu Asp  
650 655 660

Thr Thr Val Leu Ile Glu Thr Lys Arg Asp Tyr Ser Thr Glu Leu  
665 670 675

Ser Val Thr Ile Ala Val Gly Ala Ser Leu Leu Phe Leu Asn Ile  
680 685 690

Leu Ala Phe Ala Ala Leu Tyr Tyr Lys Lys Asp Lys Arg Arg His  
695 700 705

Glu Thr His Arg Arg Pro Ser Pro Gln Arg Asn Thr Thr Asn Asp  
710 715 720

Ile Ala His Ile Gln Asn Glu Glu Ile Met Ser Leu Gln Met Lys  
725 730 735

Gln Leu Glu His Asp His Glu Cys Glu Ser Leu Gln Ala His Asp  
740 745 750

Thr Leu Arg Leu Thr Cys Pro Pro Asp Tyr Thr Leu Thr Leu Arg  
755 760 765

Arg Ser Pro Asp Asp Ile Pro Leu Met Thr Pro Asn Thr Ile Thr  
770 775 780

Met Ile Pro Asn Thr Leu Thr Gly Met Gln Pro Leu His Thr Phe  
785 790 795

Asn Thr Phe Ser Gly Gly Gln Asn Ser Thr Asn Leu Pro His Gly  
800 805 810

His Ser Thr Thr Arg Val  
815

<210> 376

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 376

ggcaagctac ggaaacgtca tcgtg 25

<210> 377

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 377

aacccccgag ccaaaagatg gtcac 25

<210> 378

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 378

gtaccggtga ccaggcagca aaaggcaact atgggctcct ggatcag 47

<210> 379

<211> 2461

<212> DNA

<213> Homo sapiens

<400> 379

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ggcgaatgtt gtcggctcgg gatgggtcca ggatgttact ccttcttctt 100

ttgttgggggt ctgggcagggt gccacagcaa gtcggggcgg gtcaaacgtt 150

cgagtacttg aaacgggagc actcgctgtc gaagccctac cagggtgtgg 200

gcacaggcag ttctcactg tggaatctga tgggcaatgc catggtgatg 250

accagatata tccgccttac ccagatatg caaagtaaac aggggtgcctt 300

gtggaaccgg gtgcatgtt tctgagaga ctgggagttg cagggtgact 350

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atctgttaca caaaggatcg gatgcagcca gggccttgtt ttggaacat 450

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ccttccatgt gggagcagag gtgtgaagag aatttacgtg gttgtgatgc 1350

caaatcaca gaacagaatt tcatagcca ggctgccgtg ttgttgact 1400

cagaaggccc ttctactca gtttgaatc cacaagaat taaaactgg 1450

taacaccaca ggctttctga ccatccattc gtgggtttt gcattgacc 1500

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ggatgccatg gattagctgt gcaactgacc agctccaggt ttgatcaaac 1900

caaaagcaac attgtcatg tggctgacc atgtggagat gttctggac 1950

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 ggccgcatg g 2461

<210> 380  
 <211> 348  
 <212> PRT  
 <213> Homo sapiens

<400> 380  
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 Leu Leu Leu Gly Ser Gly Gln Gly Pro Gln Gln Val Gly Ala Gly  
 35 40 45  
 Gln Thr Phe Glu Tyr Leu Lys Arg Glu His Ser Leu Ser Lys Pro  
 50 55 60  
 Tyr Gln Gly Val Gly Thr Gly Ser Ser Ser Leu Trp Asn Leu Met  
 65 70 75  
 Gly Asn Ala Met Val Met Thr Gln Tyr Ile Arg Leu Thr Pro Asp  
 80 85 90  
 Met Gln Ser Lys Gln Gly Ala Leu Trp Asn Arg Val Pro Cys Phe  
 95 100 105

Leu Arg Asp Trp Glu Leu Gln Val His Phe Lys Ile His Gly Gln  
110 115 120

Gly Lys Lys Asn Leu His Gly Asp Gly Leu Ala Ile Trp Tyr Thr  
125 130 135

Lys Asp Arg Met Gln Pro Gly Pro Val Phe Gly Asn Met Asp Lys  
140 145 150

Phe Val Gly Leu Gly Val Phe Val Asp Thr Tyr Pro Asn Glu Glu  
155 160 165

Lys Gln Gln Glu Arg Val Phe Pro Tyr Ile Ser Ala Met Val Asn  
170 175 180

Asn Gly Ser Leu Ser Tyr Asp His Glu Arg Asp Gly Arg Pro Thr  
185 190 195

Glu Leu Gly Gly Cys Thr Ala Ile Val Arg Asn Leu His Tyr Asp  
200 205 210

Thr Phe Leu Val Ile Arg Tyr Val Lys Arg His Leu Thr Ile Met  
215 220 225

Met Asp Ile Asp Gly Lys His Glu Trp Arg Asp Cys Ile Glu Val  
230 235 240

Pro Gly Val Arg Leu Pro Arg Gly Tyr Tyr Phe Gly Thr Ser Ser  
245 250 255

Ile Thr Gly Asp Leu Ser Asp Asn His Asp Val Ile Ser Leu Lys  
260 265 270

Leu Phe Glu Leu Thr Val Glu Arg Thr Pro Glu Glu Glu Lys Leu  
275 280 285

His Arg Asp Val Phe Leu Pro Ser Val Asp Asn Met Lys Leu Pro  
290 295 300

Glu Met Thr Ala Pro Leu Pro Pro Leu Ser Gly Leu Ala Leu Phe  
305 310 315

Leu Ile Val Phe Phe Ser Leu Val Phe Ser Val Phe Ala Ile Val  
320 325 330



Ile Gly Ile Ile Leu Tyr Asn Lys Trp Gln Glu Gln Ser Arg Lys  
335 340 345

Arg Phe Tyr

<210> 381

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 381

ccttgggtcg tggcagcagt gg 22

<210> 382

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 382

cactctccag gctgcatgct cagg 24

<210> 383

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 383

gtcaaacgtt cgagtacttg aaacgggagc actcgtgtc gaagc 45

<210> 384

<211> 3150

<212> DNA

<213> Homo sapiens

<400> 384

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ggggactcca agatttccat gaagaaaatc agttgtcttc attcaagaat 150  
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<210> 385

<211> 480

<212> PRT

<213> Homo sapiens

<400> 385

Met Leu Phe Arg Asn Arg Phe Leu Leu Leu Leu Ala Leu Ala Ala

1 5 10 15

Leu Leu Ala Phe Val Ser Leu Ser Leu Gln Phe Phe His Leu Ile

20 25 30

Pro Val Ser Thr Pro Lys Asn Gly Met Ser Ser Lys Ser Arg Lys  
35 40 45

Arg Ile Met Pro Asp Pro Val Thr Glu Pro Pro Val Thr Asp Pro  
50 55 60

Val Tyr Glu Ala Leu Leu Tyr Cys Asn Ile Pro Ser Val Ala Glu  
65 70 75

Arg Ser Met Glu Gly His Ala Pro His His Phe Lys Leu Val Ser  
80 85 90

Val His Val Phe Ile Arg His Gly Asp Arg Tyr Pro Leu Tyr Val  
95 100 105

Ile Pro Lys Thr Lys Arg Pro Glu Ile Asp Cys Thr Leu Val Ala  
110 115 120

Asn Arg Lys Pro Tyr His Pro Lys Leu Glu Ala Phe Ile Ser His  
125 130 135

Met Ser Lys Gly Ser Gly Ala Ser Phe Glu Ser Pro Leu Asn Ser  
140 145 150

Leu Pro Leu Tyr Pro Asn His Pro Leu Cys Glu Met Gly Glu Leu  
155 160 165

Thr Gln Thr Gly Val Val Gln His Leu Gln Asn Gly Gln Leu Leu  
170 175 180

Arg Asp Ile Tyr Leu Lys Lys His Lys Leu Leu Pro Asn Asp Trp  
185 190 195

Ser Ala Asp Gln Leu Tyr Leu Glu Thr Thr Gly Lys Ser Arg Thr  
200 205 210

Leu Gln Ser Gly Leu Ala Leu Leu Tyr Gly Phe Leu Pro Asp Phe  
215 220 225

Asp Trp Lys Lys Ile Tyr Phe Arg His Gln Pro Ser Ala Leu Phe  
230 235 240

Cys Ser Gly Ser Cys Tyr Cys Pro Val Arg Asn Gln Tyr Leu Glu  
245 250 255

Lys Glu Gln Arg Arg Gln Tyr Leu Leu Arg Leu Lys Asn Ser Gln  
260 265 270

Leu Glu Lys Thr Tyr Gly Glu Met Ala Lys Ile Val Asp Val Pro  
275 280 285

Thr Lys Gln Leu Arg Ala Ala Asn Pro Ile Asp Ser Met Leu Cys  
290 295 300

His Phe Cys His Asn Val Ser Phe Pro Cys Thr Arg Asn Gly Cys  
305 310 315

Val Asp Met Glu His Phe Lys Val Ile Lys Thr His Gln Ile Glu  
320 325 330

Asp Glu Arg Glu Arg Arg Glu Lys Lys Leu Tyr Phe Gly Tyr Ser  
335 340 345

Leu Leu Gly Ala His Pro Ile Leu Asn Gln Thr Ile Gly Arg Met  
350 355 360

Gln Arg Ala Thr Glu Gly Arg Lys Glu Glu Leu Phe Ala Leu Tyr  
365 370 375

Ser Ala His Asp Val Thr Leu Ser Pro Val Leu Ser Ala Leu Gly  
380 385 390

Leu Ser Glu Ala Arg Phe Pro Arg Phe Ala Ala Arg Leu Ile Phe  
395 400 405

Glu Leu Trp Gln Asp Arg Glu Lys Pro Ser Glu His Ser Val Arg  
410 415 420

Ile Leu Tyr Asn Gly Val Asp Val Thr Phe His Thr Ser Phe Cys  
425 430 435

Gln Asp His His Lys Arg Ser Pro Lys Pro Met Cys Pro Leu Glu  
440 445 450

Asn Leu Val Arg Phe Val Lys Arg Asp Met Phe Val Ala Leu Gly  
455 460 465

Gly Ser Gly Thr Asn Tyr Tyr Asp Ala Cys His Arg Glu Gly Phe  
470 475 480

<210> 386

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 386

ccaagcagct tagagctcca gacc 24

<210> 387

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 387

ttccctatgc tctgtattgg catgg 25

<210> 388

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 388

gccacttctg ccacaatgtc agctttccct gtaccagaaa tggctgtgtt 50

<210> 389

<211> 3313

<212> DNA

<213> Homo sapiens

<400> 389

aaaaaagctc actaaagttt ctattagagc gaatacggta gatttccatc 50

cccttttgaa gaacagtact gtggagctat ttaagagata aaaacgaaat 100

atcctttctg ggagtcaag attgtgcagt aattggttag gactctgagc 150

gccgctgttc accaatcggg gagagaaaag cggagatcct gctcgccttg 200  
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 aaactctatc tca 3313

<210> 390

<211> 916

<212> PRT

<213> Homo sapiens

<400> 390

Met Ile Pro Ala Arg Leu His Arg Asp Tyr Lys Gly Leu Val Leu

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15

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20 25 30

Ile Arg Tyr Ser Val Pro Glu Glu Leu Glu Lys Gly Ser Arg Val  
35 40 45

Gly Asp Ile Ser Arg Asp Leu Gly Leu Glu Pro Arg Glu Leu Ala  
50 55 60

Glu Arg Gly Val Arg Ile Ile Pro Arg Gly Arg Thr Gln Leu Phe  
65 70 75

Ala Leu Asn Pro Arg Ser Gly Ser Leu Val Thr Ala Gly Arg Ile  
80 85 90

Asp Arg Glu Glu Leu Cys Met Gly Ala Ile Lys Cys Gln Leu Asn  
95 100 105

Leu Asp Ile Leu Met Glu Asp Lys Val Lys Ile Tyr Gly Val Glu  
110 115 120

Val Glu Val Arg Asp Ile Asn Asp Asn Ala Pro Tyr Phe Arg Glu  
125 130 135

Ser Glu Leu Glu Ile Lys Ile Ser Glu Asn Ala Ala Thr Glu Met  
140 145 150

Arg Phe Pro Leu Pro His Ala Trp Asp Pro Asp Ile Gly Lys Asn  
155 160 165

Ser Leu Gln Ser Tyr Glu Leu Ser Pro Asn Thr His Phe Ser Leu  
170 175 180

Ile Val Gln Asn Gly Ala Asp Gly Ser Lys Tyr Pro Glu Leu Val  
185 190 195

Leu Lys Arg Ala Leu Asp Arg Glu Glu Lys Ala Ala His His Leu  
200 205 210

Val Leu Thr Ala Ser Asp Gly Gly Asp Pro Val Arg Thr Gly Thr  
215 220 225

Ala Arg Ile Arg Val Met Val Leu Asp Ala Asn Asp Asn Ala Pro  
230 235 240

Ala Phe Ala Gln Pro Glu Tyr Arg Ala Ser Val Pro Glu Asn Leu  
245 250 255

Ala Leu Gly Thr Gln Leu Leu Val Val Asn Ala Thr Asp Pro Asp  
260 265 270

Glu Gly Val Asn Ala Glu Val Arg Tyr Ser Phe Arg Tyr Val Asp  
275 280 285

Asp Lys Ala Ala Gln Val Phe Lys Leu Asp Cys Asn Ser Gly Thr  
290 295 300

Ile Ser Thr Ile Gly Glu Leu Asp His Glu Glu Ser Gly Phe Tyr  
305 310 315

Gln Met Glu Val Gln Ala Met Asp Asn Ala Gly Tyr Ser Ala Arg  
320 325 330

Ala Lys Val Leu Ile Thr Val Leu Asp Val Asn Asp Asn Ala Pro  
335 340 345

Glu Val Val Leu Thr Ser Leu Ala Ser Ser Val Pro Glu Asn Ser  
350 355 360

Pro Arg Gly Thr Leu Ile Ala Leu Leu Asn Val Asn Asp Gln Asp  
365 370 375

Ser Glu Glu Asn Gly Gln Val Ile Cys Phe Ile Gln Gly Asn Leu  
380 385 390

Pro Phe Lys Leu Glu Lys Ser Tyr Gly Asn Tyr Tyr Ser Leu Val  
395 400 405

Thr Asp Ile Val Leu Asp Arg Glu Gln Val Pro Ser Tyr Asn Ile  
410 415 420

Thr Val Thr Ala Thr Asp Arg Gly Thr Pro Pro Leu Ser Thr Glu  
425 430 435

Thr His Ile Ser Leu Asn Val Ala Asp Thr Asn Asp Asn Pro Pro  
440 445 450

Val Phe Pro Gln Ala Ser Tyr Ser Ala Tyr Ile Pro Glu Asn Asn  
455 460 465

Pro Arg Gly Val Ser Leu Val Ser Val Thr Ala His Asp Pro Asp  
470 475 480

Cys Glu Glu Asn Ala Gln Ile Thr Tyr Ser Leu Ala Glu Asn Thr  
485 490 495

Ile Gln Gly Ala Ser Leu Ser Ser Tyr Val Ser Ile Asn Ser Asp  
500 505 510

Thr Gly Val Leu Tyr Ala Leu Ser Ser Phe Asp Tyr Glu Gln Phe  
515 520 525

Arg Asp Leu Gln Val Lys Val Met Ala Arg Asp Asn Gly His Pro  
530 535 540

Pro Leu Ser Ser Asn Val Ser Leu Ser Leu Phe Val Leu Asp Gln  
545 550 555

Asn Asp Asn Ala Pro Glu Ile Leu Tyr Pro Ala Leu Pro Thr Asp  
560 565 570

Gly Ser Thr Gly Val Glu Leu Ala Pro Arg Ser Ala Glu Pro Gly  
575 580 585

Tyr Leu Val Thr Lys Val Val Ala Val Asp Arg Asp Ser Gly Gln  
590 595 600

Asn Ala Trp Leu Ser Tyr Arg Leu Leu Lys Ala Ser Glu Pro Gly  
605 610 615

Leu Phe Ser Val Gly Leu His Thr Gly Glu Val Arg Thr Ala Arg  
620 625 630

Ala Leu Leu Asp Arg Asp Ala Leu Lys Gln Ser Leu Val Val Ala  
635 640 645

Val Gln Asp His Gly Gln Pro Pro Leu Ser Ala Thr Val Thr Leu  
650 655 660

Thr Val Ala Val Ala Asp Ser Ile Pro Gln Val Leu Ala Asp Leu  
665 670 675

Gly Ser Leu Glu Ser Pro Ala Asn Ser Glu Thr Ser Asp Leu Thr  
680 685 690

Leu Tyr Leu Val Val Ala Val Ala Ala Val Ser Cys Val Phe Leu  
695 700 705

Ala Phe Val Ile Leu Leu Leu Ala Leu Arg Leu Arg Arg Trp His  
710 715 720

Lys Ser Arg Leu Leu Gln Ala Ser Gly Gly Gly Leu Thr Gly Ala  
725 730 735

Pro Ala Ser His Phe Val Gly Val Asp Gly Val Gln Ala Phe Leu  
740 745 750

Gln Thr Tyr Ser His Glu Val Ser Leu Thr Thr Asp Ser Arg Lys  
755 760 765

Ser His Leu Ile Phe Pro Gln Pro Asn Tyr Ala Asp Met Leu Val  
770 775 780

Ser Gln Glu Ser Phe Glu Lys Ser Glu Pro Leu Leu Leu Ser Gly  
785 790 795

Asp Ser Val Phe Ser Lys Asp Ser His Gly Leu Ile Glu Val Ser  
800 805 810

Leu Tyr Gln Ile Phe Phe Leu Phe Phe Phe Asn Cys Ser Val Ser  
815 820 825

Gln Ala Gly Val Gln Arg Tyr Asp His Ser Ser Leu Arg Pro Gln  
830 835 840

Thr Pro Arg Leu Lys Gln Leu Ser His Leu Cys Leu Arg Cys Asn  
845 850 855

Arg Asp Tyr Arg Cys Lys Pro Pro Thr Val Cys Leu Ser Ile Tyr  
860 865 870

Leu Ser Ile Tyr Leu Ser Ile Tyr Leu Ser Ile Tyr Leu Leu Leu  
875 880 885

Ser Cys Thr Asp Gly Ser Leu Thr Pro Val Ile Pro Val Leu Trp  
890 895 900

Glu Ala Glu Ala Gly Gly Ser Pro Glu Val Gly Ser Leu Arg Pro  
905 910 915

Ala

<210> 391

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 391

tccgtctctg tgaaccgccc cac 23

<210> 392

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 392

ctcgggcgca ttgtcgttct ggtc 24

<210> 393

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 393

ccgactgtga aagagaacgc cccagatcca ctgttcccc 40

<210> 394

<211> 999

<212> DNA

<213> Homo sapiens

<400> 394

cccaggctct agtcaggag gagaaggagg aggagcagga ggtggagatt 50

cccagtaaa aggctccaga atcgtgtacc aggcagagaa ctgaagtact 100

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 ctggaagacc tcaccatggg acgccccga cctcgtgcgg ccaagacgtg 200  
 gatgttcctg ctcttgctgg ggggagcctg ggcaggacac tccagggcac 250  
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 cgatgtggag gaccacaacc atgatctgat gcttctcaa ctgcgtgacc 550  
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 gctcagacct ctgtgggagg tccgacaaac ctggcgtcta taccaacatc 900  
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<210> 395

<211> 260

<212> PRT

<213> Homo sapiens

<400> 395

Met Gly Arg Pro Arg Pro Arg Ala Ala Lys Thr Trp Met Phe Leu

1

5

10

15



Leu Leu Leu Gly Gly Ala Trp Ala Gly His Ser Arg Ala Gln Glu  
20 25 30

Asp Lys Val Leu Gly Gly His Glu Cys Gln Pro His Ser Gln Pro  
35 40 45

Trp Gln Ala Ala Leu Phe Gln Gly Gln Gln Leu Leu Cys Gly Gly  
50 55 60

Val Leu Val Gly Gly Asn Trp Val Leu Thr Ala Ala His Cys Lys  
65 70 75

Lys Pro Lys Tyr Thr Val Arg Leu Gly Asp His Ser Leu Gln Asn  
80 85 90

Lys Asp Gly Pro Glu Gln Glu Ile Pro Val Val Gln Ser Ile Pro  
95 100 105

His Pro Cys Tyr Asn Ser Ser Asp Val Glu Asp His Asn His Asp  
110 115 120

Leu Met Leu Leu Gln Leu Arg Asp Gln Ala Ser Leu Gly Ser Lys  
125 130 135

Val Lys Pro Ile Ser Leu Ala Asp His Cys Thr Gln Pro Gly Gln  
140 145 150

Lys Cys Thr Val Ser Gly Trp Gly Thr Val Thr Ser Pro Arg Glu  
155 160 165

Asn Phe Pro Asp Thr Leu Asn Cys Ala Glu Val Lys Ile Phe Pro  
170 175 180

Gln Lys Lys Cys Glu Asp Ala Tyr Pro Gly Gln Ile Thr Asp Gly  
185 190 195

Met Val Cys Ala Gly Ser Ser Lys Gly Ala Asp Thr Cys Gln Gly  
200 205 210

Asp Ser Gly Gly Pro Leu Val Cys Asp Gly Ala Leu Gln Gly Ile  
215 220 225

Thr Ser Trp Gly Ser Asp Pro Cys Gly Arg Ser Asp Lys Pro Gly  
230 235 240

Val Tyr Thr Asn Ile Cys Arg Tyr Leu Asp Trp Ile Lys Lys Ile  
245 250 255

Ile Gly Ser Lys Gly  
260

<210> 396

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 396

cagcctacag aataaagatg gccc 24

<210> 397

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 397

ggtgcaatga tctgccaggc tgat 24

<210> 398

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 398

agaaatacct gtggttcagt ccataccaaa cccctgctac aacagcag 48

<210> 399

<211> 2236

<212> DNA

<213> Homo sapiens

<400> 399

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gccgcgagg ccccgcccc gcccgcccc gcccgcccc ggccggcggg 200  
ggaaccgggc ggattcctcg cgcgtcaaac cacctgatcc cataaaacat 250  
tcatectccc ggcggccgc gctgcgagcg ccccgccagt ccgcgccgcc 300  
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cccagccaga gccgggaggga gcggagcgcg ccgagcctcg tcccgcggcc 400  
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<211> 473

<212> PRT

<213> Homo sapiens

<400> 400

Met Lys Arg Ala Ser Ala Gly Gly Ser Arg Leu Leu Ala Trp Val  
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Leu Trp Leu Gln Ala Trp Gln Val Ala Ala Pro Cys Pro Gly Ala  
20 25 30

Cys Val Cys Tyr Asn Glu Pro Lys Val Thr Thr Ser Cys Pro Gln  
35 40 45

Gln Gly Leu Gln Ala Val Pro Val Gly Ile Pro Ala Ala Ser Gln  
50 55 60

Arg Ile Phe Leu His Gly Asn Arg Ile Ser His Val Pro Ala Ala  
65 70 75

Ser Phe Arg Ala Cys Arg Asn Leu Thr Ile Leu Trp Leu His Ser  
80 85 90

Asn Val Leu Ala Arg Ile Asp Ala Ala Ala Phe Thr Gly Leu Ala  
95 100 105

Leu Leu Glu Gln Leu Asp Leu Ser Asp Asn Ala Gln Leu Arg Ser  
110 115 120

Val Asp Pro Ala Thr Phe His Gly Leu Gly Arg Leu His Thr Leu  
125 130 135

His Leu Asp Arg Cys Gly Leu Gln Glu Leu Gly Pro Gly Leu Phe  
140 145 150

Arg Gly Leu Ala Ala Leu Gln Tyr Leu Tyr Leu Gln Asp Asn Ala  
155 160 165

Leu Gln Ala Leu Pro Asp Asp Thr Phe Arg Asp Leu Gly Asn Leu  
170 175 180

Thr His Leu Phe Leu His Gly Asn Arg Ile Ser Ser Val Pro Glu  
185 190 195

Arg Ala Phe Arg Gly Leu His Ser Leu Asp Arg Leu Leu Leu His

200	205	210
Gln Asn Arg Val Ala His Val His Pro His Ala Phe Arg Asp Leu		
215	220	225
Gly Arg Leu Met Thr Leu Tyr Leu Phe Ala Asn Asn Leu Ser Ala		
230	235	240
Leu Pro Thr Glu Ala Leu Ala Pro Leu Arg Ala Leu Gln Tyr Leu		
245	250	255
Arg Leu Asn Asp Asn Pro Trp Val Cys Asp Cys Arg Ala Arg Pro		
260	265	270
Leu Trp Ala Trp Leu Gln Lys Phe Arg Gly Ser Ser Ser Glu Val		
275	280	285
Pro Cys Ser Leu Pro Gln Arg Leu Ala Gly Arg Asp Leu Lys Arg		
290	295	300
Leu Ala Ala Asn Asp Leu Gln Gly Cys Ala Val Ala Thr Gly Pro		
305	310	315
Tyr His Pro Ile Trp Thr Gly Arg Ala Thr Asp Glu Glu Pro Leu		
320	325	330
Gly Leu Pro Lys Cys Cys Gln Pro Asp Ala Ala Asp Lys Ala Ser		
335	340	345
Val Leu Glu Pro Gly Arg Pro Ala Ser Ala Gly Asn Ala Leu Lys		
350	355	360
Gly Arg Val Pro Pro Gly Asp Ser Pro Pro Gly Asn Gly Ser Gly		
365	370	375
Pro Arg His Ile Asn Asp Ser Pro Phe Gly Thr Leu Pro Gly Ser		
380	385	390
Ala Glu Pro Pro Leu Thr Ala Val Arg Pro Glu Gly Ser Glu Pro		
395	400	405
Pro Gly Phe Pro Thr Ser Gly Pro Arg Arg Arg Pro Gly Cys Ser		
410	415	420
Arg Lys Asn Arg Thr Arg Ser His Cys Arg Leu Gly Gln Ala Gly		

425                      430                      435

Ser Gly Gly Gly Gly Thr Gly Asp Ser Glu Gly Ser Gly Ala Leu  
440                      445                      450

Pro Ser Leu Thr Cys Ser Leu Thr Pro Leu Gly Leu Ala Leu Val  
455                      460                      465

Leu Trp Thr Val Leu Gly Pro Cys  
470

<210> 401

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 401

tggctgccct gcagtacctc tacc 24

<210> 402

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 402

ccctgcaggt cattggcagc tagg 24

<210> 403

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 403

aggcactgcc tgatgacacc ttccgcgacc tgggcaacct cacac 45

<210> 404

<211> 2738

<212> DNA

<213> Homo sapiens

<400> 404

ggaagtccac ggggagcttg gatgccaaag ggaggacggc tgggtcctct 50  
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agctgaatcc agcaagaaca atggaggcca gcgggaagct cattgcaga 200  
caaaggcaag tccttttttc ctttctcctt ttgggcttat ctctggcggg 250  
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 tgttttaag tgaacattta cctttattcc tggttctt 2738

<210> 405

<211> 798

<212> PRT

<213> Homo sapiens

<400> 405

Met Glu Ala Ser Gly Lys Leu Ile Cys Arg Gln Arg Gln Val Leu

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Phe Ser Phe Leu Leu Leu Gly Leu Ser Leu Ala Gly Ala Ala Glu

20 25 30

Pro Arg Ser Tyr Ser Val Val Glu Glu Thr Glu Gly Ser Ser Phe

35 40 45

Val Thr Asn Leu Ala Lys Asp Leu Gly Leu Glu Gln Arg Glu Phe

50 55 60

Ser Arg Arg Gly Val Arg Val Val Ser Arg Gly Asn Lys Leu His

65 70 75

Leu Gln Leu Asn Gln Glu Thr Ala Asp Leu Leu Leu Asn Glu Lys  
80 85 90

Leu Asp Arg Glu Asp Leu Cys Gly His Thr Glu Pro Cys Val Leu  
95 100 105

Arg Phe Gln Val Leu Leu Glu Ser Pro Phe Glu Phe Phe Gln Ala  
110 115 120

Glu Leu Gln Val Ile Asp Ile Asn Asp His Ser Pro Val Phe Leu  
125 130 135

Asp Lys Gln Met Leu Val Lys Val Ser Glu Ser Ser Pro Pro Gly  
140 145 150

Thr Thr Phe Pro Leu Lys Asn Ala Glu Asp Leu Asp Val Gly Gln  
155 160 165

Asn Asn Ile Glu Asn Tyr Ile Ile Ser Pro Asn Ser Tyr Phe Arg  
170 175 180

Val Leu Thr Arg Lys Arg Ser Asp Gly Arg Lys Tyr Pro Glu Leu  
185 190 195

Val Leu Asp Lys Ala Leu Asp Arg Glu Glu Glu Ala Glu Leu Arg  
200 205 210

Leu Thr Leu Thr Ala Leu Asp Gly Gly Ser Pro Pro Arg Ser Gly  
215 220 225

Thr Ala Gln Val Tyr Ile Glu Val Leu Asp Val Asn Asp Asn Ala  
230 235 240

Pro Glu Phe Glu Gln Pro Phe Tyr Arg Val Gln Ile Ser Glu Asp  
245 250 255

Ser Pro Val Gly Phe Leu Val Val Lys Val Ser Ala Thr Asp Val  
260 265 270

Asp Thr Gly Val Asn Gly Glu Ile Ser Tyr Ser Leu Phe Gln Ala  
275 280 285

Ser Glu Glu Ile Gly Lys Thr Phe Lys Ile Asn Pro Leu Thr Gly  
290 295 300

Glu Ile Glu Leu Lys Lys Gln Leu Asp Phe Glu Lys Leu Gln Ser  
305 310 315

Tyr Glu Val Asn Ile Glu Ala Arg Asp Ala Gly Thr Phe Ser Gly  
320 325 330

Lys Cys Thr Val Leu Ile Gln Val Ile Asp Val Asn Asp His Ala  
335 340 345

Pro Glu Val Thr Met Ser Ala Phe Thr Ser Pro Ile Pro Glu Asn  
350 355 360

Ala Pro Glu Thr Val Val Ala Leu Phe Ser Val Ser Asp Leu Asp  
365 370 375

Ser Gly Glu Asn Gly Lys Ile Ser Cys Ser Ile Gln Glu Asp Leu  
380 385 390

Pro Phe Leu Leu Lys Ser Ala Glu Asn Phe Tyr Thr Leu Leu Thr  
395 400 405

Glu Arg Pro Leu Asp Arg Glu Ser Arg Ala Glu Tyr Asn Ile Thr  
410 415 420

Ile Thr Val Thr Asp Leu Gly Thr Pro Met Leu Ile Thr Gln Leu  
425 430 435

Asn Met Thr Val Leu Ile Ala Asp Val Asn Asp Asn Ala Pro Ala  
440 445 450

Phe Thr Gln Thr Ser Tyr Thr Leu Phe Val Arg Glu Asn Asn Ser  
455 460 465

Pro Ala Leu His Ile Arg Ser Val Ser Ala Thr Asp Arg Asp Ser  
470 475 480

Gly Thr Asn Ala Gln Val Thr Tyr Ser Leu Leu Pro Pro Gln Asp  
485 490 495

Pro His Leu Pro Leu Thr Ser Leu Val Ser Ile Asn Ala Asp Asn  
500 505 510

Gly His Leu Phe Ala Leu Arg Ser Leu Asp Tyr Glu Ala Leu Gln  
515 520 525

Gly Phe Gln Phe Arg Val Gly Ala Ser Asp His Gly Ser Pro Ala  
530 535 540

Leu Ser Ser Glu Ala Leu Val Arg Val Val Val Leu Asp Ala Asn  
545 550 555

Asp Asn Ser Pro Phe Val Leu Tyr Pro Leu Gln Asn Gly Ser Ala  
560 565 570

Pro Cys Thr Glu Leu Val Pro Arg Ala Ala Glu Pro Gly Tyr Leu  
575 580 585

Val Thr Lys Val Val Ala Val Asp Gly Asp Ser Gly Gln Asn Ala  
590 595 600

Trp Leu Ser Tyr Gln Leu Leu Lys Ala Thr Glu Leu Gly Leu Phe  
605 610 615

Gly Val Trp Ala His Asn Gly Glu Val Arg Thr Ala Arg Leu Leu  
620 625 630

Ser Glu Arg Asp Ala Ala Lys His Arg Leu Val Val Leu Val Lys  
635 640 645

Asp Asn Gly Glu Pro Pro Arg Ser Ala Thr Ala Thr Leu His Val  
650 655 660

Leu Leu Val Asp Gly Phe Ser Gln Pro Tyr Leu Pro Leu Pro Glu  
665 670 675

Ala Ala Pro Thr Gln Ala Gln Ala Asp Leu Leu Thr Val Tyr Leu  
680 685 690

Val Val Ala Leu Ala Ser Val Ser Ser Leu Phe Leu Phe Ser Val  
695 700 705

Leu Leu Phe Val Ala Val Arg Leu Cys Arg Arg Ser Arg Ala Ala  
710 715 720

Ser Val Gly Arg Cys Leu Val Pro Glu Gly Pro Leu Pro Gly His  
725 730 735

Leu Val Asp Met Ser Gly Thr Arg Thr Leu Ser Gln Ser Tyr Gln  
740 745 750

Tyr Glu Val Cys Leu Ala Gly Gly Ser Gly Thr Asn Glu Phe Lys  
755 760 765

Phe Leu Lys Pro Ile Ile Pro Asn Phe Pro Pro Gln Cys Pro Gly  
770 775 780

Lys Glu Ile Gln Gly Asn Ser Thr Phe Pro Asn Asn Phe Gly Phe  
785 790 795

Asn Ile Gln

<210> 406

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 406

ctgagaacgc gcctgaaact gtg 23

<210> 407

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 407

agcgttgatc ttgacatcgg cg 22

<210> 408

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 408

ttagttgctc cattcaggag gatctaccct tcctcctgaa atccgcggaa 50

<210> 409  
<211> 1379  
<212> DNA  
<213> Homo sapiens

<400> 409  
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cggtcgacga ccgccccgcg tcatcgggct cctcggctgg tggcaagtat 150  
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agtgtgcgt tatggtcaga ggagcagcct gtcaccctc tccaggtggg 250  
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caaggtgcaa cgtccgagag agccttttct ctctggatgg cgctggagca 500  
cacttccctg acagagaaga ggagtattac acagagccag aagtggcgga 550  
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aactcaagcc gaccaaatag gccctcttcc cagcacttg ataaaaagtg 1050

tggactgggt gcttgattt tcctattct tttaattag ttattatg 1100

tatgctacca ttcgaactga gatttcgg tggctaattc caggacaaga 1150

gcaggaacat gtggagtagt gatggtctga aagaagttg aaagaggaac 1200

ttcaatcctt cgttcagaa attagtgcta cagttcata catttctcc 1250

agtgcgtgt tgacttgaaa cttcaggcag attaaaagaa tcattgttg 1300

aacaactgaa tgtataaaaa aattataaac tgggtttta actagtattg 1350

caataagcaa atgcaaaaat attcaatag 1379

<210> 410

<211> 360

<212> PRT

<213> Homo sapiens

<400> 410

Met Val Pro Ala Ala Gly Arg Arg Pro Pro Arg Val Met Arg Leu

1 5 10 15

Leu Gly Trp Trp Gln Val Leu Leu Trp Val Leu Gly Leu Pro Val

20 25 30

Arg Gly Val Glu Val Ala Glu Glu Ser Gly Arg Leu Trp Ser Glu

35 40 45

Glu Gln Pro Ala His Pro Leu Gln Val Gly Ala Val Tyr Leu Gly

50 55 60

Glu Glu Glu Leu Leu His Asp Pro Met Gly Gln Asp Arg Ala Ala

65 70 75

Glu Glu Ala Asn Ala Val Leu Gly Leu Asp Thr Gln Gly Asp His

80 85 90

Met Val Met Leu Ser Val Ile Pro Gly Glu Ala Glu Asp Lys Val

95 100 105

Ser Ser Glu Pro Ser Gly Val Thr Cys Gly Ala Gly Gly Ala Glu

110 115 120



Asp Ser Arg Cys Asn Val Arg Glu Ser Leu Phe Ser Leu Asp Gly  
125 130 135

Ala Gly Ala His Phe Pro Asp Arg Glu Glu Glu Tyr Tyr Thr Glu  
140 145 150

Pro Glu Val Ala Glu Ser Asp Ala Ala Pro Thr Glu Asp Ser Asn  
155 160 165

Asn Thr Glu Ser Leu Lys Ser Pro Lys Val Asn Cys Glu Glu Arg  
170 175 180

Asn Ile Thr Gly Leu Glu Asn Phe Thr Leu Lys Ile Leu Asn Met  
185 190 195

Ser Gln Asp Leu Met Asp Phe Leu Asn Pro Asn Gly Ser Asp Cys  
200 205 210

Thr Leu Val Leu Phe Tyr Thr Pro Trp Cys Arg Phe Ser Ala Ser  
215 220 225

Leu Ala Pro His Phe Asn Ser Leu Pro Arg Ala Phe Pro Ala Leu  
230 235 240

His Phe Leu Ala Leu Asp Ala Ser Gln His Ser Ser Leu Ser Thr  
245 250 255

Arg Phe Gly Thr Val Ala Val Pro Asn Ile Leu Leu Phe Gln Gly  
260 265 270

Ala Lys Pro Met Ala Arg Phe Asn His Thr Asp Arg Thr Leu Glu  
275 280 285

Thr Leu Lys Ile Phe Ile Phe Asn Gln Thr Gly Ile Glu Ala Lys  
290 295 300

Lys Asn Val Val Val Thr Gln Ala Asp Gln Ile Gly Pro Leu Pro  
305 310 315

Ser Thr Leu Ile Lys Ser Val Asp Trp Leu Leu Val Phe Ser Leu  
320 325 330

Phe Phe Leu Ile Ser Phe Ile Met Tyr Ala Thr Ile Arg Thr Glu  
335 340 345

Ser Ile Arg Trp Leu Ile Pro Gly Gln Glu Gln Glu His Val Glu  
350 355 360

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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 411

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<210> 412

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 412

ccacatgttc ctgctcttgc cctgg 25

<210> 413

<211> 45

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 413

cggtagtgac tgtactctag tcctgtttta caccctgtgg tgccg 45

<210> 414

<211> 1196

<212> DNA

<213> Homo sapiens

<400> 414

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<211> 295

<212> PRT

<213> Homo sapiens

<400> 415

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His Cys Cys Leu Gly Ser Ala Arg Gly Leu Phe Leu Phe Gly Gln  
20 25 30

Pro Asp Phe Ser Tyr Lys Arg Ser Asn Cys Lys Pro Ile Pro Val  
35 40 45

Asn Leu Gln Leu Cys His Gly Ile Glu Tyr Gln Asn Met Arg Leu  
50 55 60

Pro Asn Leu Leu Gly His Glu Thr Met Lys Glu Val Leu Glu Gln  
65 70 75

Ala Gly Ala Trp Ile Pro Leu Val Met Lys Gln Cys His Pro Asp  
80 85 90

Thr Lys Lys Phe Leu Cys Ser Leu Phe Ala Pro Val Cys Leu Asp  
95 100 105

Asp Leu Asp Glu Thr Ile Gln Pro Cys His Ser Leu Cys Val Gln  
110 115 120

Val Lys Asp Arg Cys Ala Pro Val Met Ser Ala Phe Gly Phe Pro  
125 130 135

Trp Pro Asp Met Leu Glu Cys Asp Arg Phe Pro Gln Asp Asn Asp  
140 145 150

Leu Cys Ile Pro Leu Ala Ser Ser Asp His Leu Leu Pro Ala Thr  
155 160 165

Glu Glu Ala Pro Lys Val Cys Glu Ala Cys Lys Asn Lys Asn Asp  
170 175 180

Asp Asp Asn Asp Ile Met Glu Thr Leu Cys Lys Asn Asp Phe Ala  
185 190 195

Leu Lys Ile Lys Val Lys Glu Ile Thr Tyr Ile Asn Arg Asp Thr

200 205 210

Lys Ile Ile Leu Glu Thr Lys Ser Lys Thr Ile Tyr Lys Leu Asn  
215 220 225

Gly Val Ser Glu Arg Asp Leu Lys Lys Ser Val Leu Trp Leu Lys  
230 235 240

Asp Ser Leu Gln Cys Thr Cys Glu Glu Met Asn Asp Ile Asn Ala  
245 250 255

Pro Tyr Leu Val Met Gly Gln Lys Gln Gly Gly Glu Leu Val Ile  
260 265 270

Thr Ser Val Lys Arg Trp Gln Lys Gly Gln Arg Glu Phe Lys Arg  
275 280 285

Ile Ser Arg Ser Ile Arg Lys Leu Gln Cys  
290 295

<210> 416

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 416

cctggctcgc tgctgctgct c 21

<210> 417

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 417

cctcacaggt gcactgcaag ctgtc 25

<210> 418

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 418

ctcttcctct ttggccagcc cgacttctcc tacaagcgca gaattgc 47

<210> 419

<211> 1830

<212> DNA

<213> Homo sapiens

<400> 419

gtggaggccg ccgacgatgg cggggccgac ggaggccgag acggggttgg 50

ccgagccccg ggccctgtgc gcgcagcggg gccaccgcac ctacgcgcgc 100

cgctgggtgt tcctgctcgc gatcagcctg ctcaactgct ccaacgccac 150

gctgtggctc agctttgcac ctgtggctga cgtcattgct gaggacttgg 200

tcctgtccat ggagcagatc aactggctgt cactggtcta cctcgtgta 250

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ccgtgcggcg accatcctgg gtgcgtggct gaactttgcc gggagtgtgc 350

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<210> 420

<211> 560

<212> PRT

<213> Homo sapiens

<400> 420

Met Ala Gly Pro Thr Glu Ala Glu Thr Gly Leu Ala Glu Pro Arg  
1 5 10 15

Ala Leu Cys Ala Gln Arg Gly His Arg Thr Tyr Ala Arg Arg Trp  
20 25 30

Val Phe Leu Leu Ala Ile Ser Leu Leu Asn Cys Ser Asn Ala Thr  
35 40 45

Leu Trp Leu Ser Phe Ala Pro Val Ala Asp Val Ile Ala Glu Asp  
50 55 60

Leu Val Leu Ser Met Glu Gln Ile Asn Trp Leu Ser Leu Val Tyr  
65 70 75

Leu Val Val Ser Thr Pro Phe Gly Val Ala Ala Ile Trp Ile Leu  
80 85 90

Asp Ser Val Gly Leu Arg Ala Ala Thr Ile Leu Gly Ala Trp Leu  
95 100 105

Asn Phe Ala Gly Ser Val Leu Arg Met Val Pro Cys Met Val Val  
110 115 120

Gly Thr Gln Asn Pro Phe Ala Phe Leu Met Gly Gly Gln Ser Leu  
125 130 135

Cys Ala Leu Ala Gln Ser Leu Val Ile Phe Ser Pro Ala Lys Leu  
140 145 150

Ala Ala Leu Trp Phe Pro Glu His Gln Arg Ala Thr Ala Asn Met  
155 160 165

Leu Ala Thr Met Ser Asn Pro Leu Gly Val Leu Val Ala Asn Val  
170 175 180

Leu Ser Pro Val Leu Val Lys Lys Gly Glu Asp Ile Pro Leu Met  
185 190 195

Leu Gly Val Tyr Thr Ile Pro Ala Gly Val Val Cys Leu Leu Ser  
200 205 210



Thr Ile Cys Leu Trp Glu Ser Val Pro Pro Thr Pro Pro Ser Ala			
215	220	225	
Gly Ala Ala Ser Ser Thr Ser Glu Lys Phe Leu Asp Gly Leu Lys			
230	235	240	
Leu Gln Leu Met Trp Asn Lys Ala Tyr Val Ile Leu Ala Val Cys			
245	250	255	
Leu Gly Gly Met Ile Gly Ile Ser Ala Ser Phe Ser Ala Leu Leu			
260	265	270	
Glu Gln Ile Leu Cys Ala Ser Gly His Ser Ser Gly Phe Ser Gly			
275	280	285	
Leu Cys Gly Ala Leu Phe Ile Thr Phe Gly Ile Leu Gly Ala Leu			
290	295	300	
Ala Leu Gly Pro Tyr Val Asp Arg Thr Lys His Phe Thr Glu Ala			
305	310	315	
Thr Lys Ile Gly Leu Cys Leu Phe Ser Leu Ala Cys Val Pro Phe			
320	325	330	
Ala Leu Val Ser Gln Leu Gln Gly Gln Thr Leu Ala Leu Ala Ala			
335	340	345	
Thr Cys Ser Leu Leu Gly Leu Phe Gly Phe Ser Val Gly Pro Val			
350	355	360	
Ala Met Glu Leu Ala Val Glu Cys Ser Phe Pro Val Gly Glu Gly			
365	370	375	
Ala Ala Thr Gly Met Ile Phe Val Leu Gly Gln Ala Glu Gly Ile			
380	385	390	
Leu Ile Met Leu Ala Met Thr Ala Leu Thr Val Arg Arg Ser Glu			
395	400	405	
Pro Ser Leu Ser Thr Cys Gln Gln Gly Glu Asp Pro Leu Asp Trp			
410	415	420	
Thr Val Ser Leu Leu Leu Met Ala Gly Leu Cys Thr Phe Phe Ser			
425	430	435	

Cys Ile Leu Ala Val Phe Phe His Thr Pro Tyr Arg Arg Leu Gln  
440 445 450

Ala Glu Ser Gly Glu Pro Pro Ser Thr Arg Asn Ala Val Gly Gly  
455 460 465

Ala Asp Ser Gly Pro Gly Val Asp Arg Gly Gly Ala Gly Arg Ala  
470 475 480

Gly Val Leu Gly Pro Ser Thr Ala Thr Pro Glu Cys Thr Ala Arg  
485 490 495

Gly Ala Ser Leu Glu Asp Pro Arg Gly Pro Gly Ser Pro His Pro  
500 505 510

Ala Cys His Arg Ala Thr Pro Arg Ala Gln Gly Pro Ala Ala Thr  
515 520 525

Asp Ala Pro Ser Arg Pro Gly Arg Leu Ala Gly Arg Val Gln Ala  
530 535 540

Ser Arg Phe Ile Asp Pro Ala Gly Ser His Ser Ser Phe Ser Ser  
545 550 555

Pro Trp Val Ile Thr  
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<210> 421

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 421

agcttctcag ccctcctgga gcag 24

<210> 422

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 422

cggtgaata aacctggacg ctgg 25

<210> 423

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 423

tatgtggacc ggaccaagca ctctactgag gccaccaaga ttg 43

<210> 424

<211> 4313

<212> DNA

<213> Homo sapiens

<400> 424

gtccacatc ctgtcaact gggtcaggtc cctcttagac cagctctgt 50

ccatcattg ctgaagtga ccaactagt cccagtagg gggtctccc 100

tggcaattct tgatggcgt ttgacatct cagatcgctt ccaatgaaga 150

tggccttgc ttggggctct gctgtttca taatcatcta actatgggac 200

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<211> 1184  
<212> PRT  
<213> Homo sapiens

<400> 425  
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Thr Val Lys Tyr Gln Val Ser Glu Glu Val Pro Ser Gly Thr Val  
35 40 45  
Ile Gly Lys Leu Ser Gln Glu Leu Gly Arg Glu Glu Arg Arg Arg  
50 55 60  
Gln Ala Gly Ala Ala Phe Gln Val Leu Gln Leu Pro Gln Ala Leu  
65 70 75  
Pro Ile Gln Val Asp Ser Glu Glu Gly Leu Leu Ser Thr Gly Arg  
80 85 90  
Arg Leu Asp Arg Glu Gln Leu Cys Arg Gln Trp Asp Pro Cys Leu  
95 100 105  
Val Ser Phe Asp Val Leu Ala Thr Gly Asp Leu Ala Leu Ile His  
110 115 120  
Val Glu Ile Gln Val Leu Asp Ile Asn Asp His Gln Pro Arg Phe  
125 130 135  
Pro Lys Gly Glu Gln Glu Leu Glu Ile Ser Glu Ser Ala Ser Leu  
140 145 150

Arg Thr Arg Ile Pro Leu Asp Arg Ala Leu Asp Pro Asp Thr Gly  
155 160 165

Pro Asn Thr Leu His Thr Tyr Thr Leu Ser Pro Ser Glu His Phe  
170 175 180

Ala Leu Asp Val Ile Val Gly Pro Asp Glu Thr Lys His Ala Glu  
185 190 195

Leu Ile Val Val Lys Glu Leu Asp Arg Glu Ile His Ser Phe Phe  
200 205 210

Asp Leu Val Leu Thr Ala Tyr Asp Asn Gly Asn Pro Pro Lys Ser  
215 220 225

Gly Thr Ser Leu Val Lys Val Asn Val Leu Asp Ser Asn Asp Asn  
230 235 240

Ser Pro Ala Phe Ala Glu Ser Ser Leu Ala Leu Glu Ile Gln Glu  
245 250 255

Asp Ala Ala Pro Gly Thr Leu Leu Ile Lys Leu Thr Ala Thr Asp  
260 265 270

Pro Asp Gln Gly Pro Asn Gly Glu Val Glu Phe Phe Leu Ser Lys  
275 280 285

His Met Pro Pro Glu Val Leu Asp Thr Phe Ser Ile Asp Ala Lys  
290 295 300

Thr Gly Gln Val Ile Leu Arg Arg Pro Leu Asp Tyr Glu Lys Asn  
305 310 315

Pro Ala Tyr Glu Val Asp Val Gln Ala Arg Asp Leu Gly Pro Asn  
320 325 330

Pro Ile Pro Ala His Cys Lys Val Leu Ile Lys Val Leu Asp Val  
335 340 345

Asn Asp Asn Ile Pro Ser Ile His Val Thr Trp Ala Ser Gln Pro  
350 355 360

Ser Leu Val Ser Glu Ala Leu Pro Lys Asp Ser Phe Ile Ala Leu  
365 370 375



Val Met Ala Asp Asp Leu Asp Ser Gly His Asn Gly Leu Val His  
380 385 390

Cys Trp Leu Ser Gln Glu Leu Gly His Phe Arg Leu Lys Arg Thr  
395 400 405

Asn Gly Asn Thr Tyr Met Leu Leu Thr Asn Ala Thr Leu Asp Arg  
410 415 420

Glu Gln Trp Pro Lys Tyr Thr Leu Thr Leu Leu Ala Gln Asp Gln  
425 430 435

Gly Leu Gln Pro Leu Ser Ala Lys Lys Gln Leu Ser Ile Gln Ile  
440 445 450

Ser Asp Ile Asn Asp Asn Ala Pro Val Phe Glu Lys Ser Arg Tyr  
455 460 465

Glu Val Ser Thr Arg Glu Asn Asn Leu Pro Ser Leu His Leu Ile  
470 475 480

Thr Ile Lys Ala His Asp Ala Asp Leu Gly Ile Asn Gly Lys Val  
485 490 495

Ser Tyr Arg Ile Gln Asp Ser Pro Val Ala His Leu Val Ala Ile  
500 505 510

Asp Ser Asn Thr Gly Glu Val Thr Ala Gln Arg Ser Leu Asn Tyr  
515 520 525

Glu Glu Met Ala Gly Phe Glu Phe Gln Val Ile Ala Glu Asp Ser  
530 535 540

Gly Gln Pro Met Leu Ala Ser Ser Val Ser Val Trp Val Ser Leu  
545 550 555

Leu Asp Ala Asn Asp Asn Ala Pro Glu Val Val Gln Pro Val Leu  
560 565 570

Ser Asp Gly Lys Ala Ser Leu Ser Val Leu Val Asn Ala Ser Thr  
575 580 585

Gly His Leu Leu Val Pro Ile Glu Thr Pro Asn Gly Leu Gly Pro  
590 595 600

Ala Gly Thr Asp Thr Pro Pro Leu Ala Thr His Ser Ser Arg Pro  
605 610 615

Phe Leu Leu Thr Thr Ile Val Ala Arg Asp Ala Asp Ser Gly Ala  
620 625 630

Asn Gly Glu Pro Leu Tyr Ser Ile Arg Asn Gly Asn Glu Ala His  
635 640 645

Leu Phe Ile Leu Asn Pro His Thr Gly Gln Leu Phe Val Asn Val  
650 655 660

Thr Asn Ala Ser Ser Leu Ile Gly Ser Glu Trp Glu Leu Glu Ile  
665 670 675

Val Val Glu Asp Gln Gly Ser Pro Pro Leu Gln Thr Arg Ala Leu  
680 685 690

Leu Arg Val Met Phe Val Thr Ser Val Asp His Leu Arg Asp Ser  
695 700 705

Ala Arg Lys Pro Gly Ala Leu Ser Met Ser Met Leu Thr Val Ile  
710 715 720

Cys Leu Ala Val Leu Leu Gly Ile Phe Gly Leu Ile Leu Ala Leu  
725 730 735

Phe Met Ser Ile Cys Arg Thr Glu Lys Lys Asp Asn Arg Ala Tyr  
740 745 750

Asn Cys Arg Glu Ala Glu Ser Thr Tyr Arg Gln Gln Pro Lys Arg  
755 760 765

Pro Gln Lys His Ile Gln Lys Ala Asp Ile His Leu Val Pro Val  
770 775 780

Leu Arg Gly Gln Ala Gly Glu Pro Cys Glu Val Gly Gln Ser His  
785 790 795

Lys Asp Val Asp Lys Glu Ala Met Met Glu Ala Gly Trp Asp Pro  
800 805 810

Cys Leu Gln Ala Pro Phe His Leu Thr Pro Thr Leu Tyr Arg Thr  
815 820 825

Leu Arg Asn Gln Gly Asn Gln Gly Ala Pro Ala Glu Ser Arg Glu  
830 835 840

Val Leu Gln Asp Thr Val Asn Leu Leu Phe Asn His Pro Arg Gln  
845 850 855

Arg Asn Ala Ser Arg Glu Asn Leu Asn Leu Pro Glu Pro Gln Pro  
860 865 870

Ala Thr Gly Gln Pro Arg Ser Arg Pro Leu Lys Val Ala Gly Ser  
875 880 885

Pro Thr Gly Arg Leu Ala Gly Asp Gln Gly Ser Glu Glu Ala Pro  
890 895 900

Gln Arg Pro Pro Ala Ser Ser Ala Thr Leu Arg Arg Gln Arg His  
905 910 915

Leu Asn Gly Lys Val Ser Pro Glu Lys Glu Ser Gly Pro Arg Gln  
920 925 930

Ile Leu Arg Ser Leu Val Arg Leu Ser Val Ala Ala Phe Ala Glu  
935 940 945

Arg Asn Pro Val Glu Glu Leu Thr Val Asp Ser Pro Pro Val Gln  
950 955 960

Gln Ile Ser Gln Leu Leu Ser Leu Leu His Gln Gly Gln Phe Gln  
965 970 975

Pro Lys Pro Asn His Arg Gly Asn Lys Tyr Leu Ala Lys Pro Gly  
980 985 990

Gly Ser Arg Ser Ala Ile Pro Asp Thr Asp Gly Pro Ser Ala Arg  
995 1000 1005

Ala Gly Gly Gln Thr Asp Pro Glu Gln Glu Glu Gly Pro Leu Asp  
1010 1015 1020

Pro Glu Glu Asp Leu Ser Val Lys Gln Leu Leu Glu Glu Glu Leu  
1025 1030 1035

Ser Ser Leu Leu Asp Pro Ser Thr Gly Leu Ala Leu Asp Arg Leu  
1040 1045 1050

Ser Ala Pro Asp Pro Ala Trp Met Ala Arg Leu Ser Leu Pro Leu  
1055 1060 1065

Thr Thr Asn Tyr Arg Asp Asn Val Ile Ser Pro Asp Ala Ala Ala  
1070 1075 1080

Thr Glu Glu Pro Arg Thr Phe Gln Thr Phe Gly Lys Ala Glu Ala  
1085 1090 1095

Pro Glu Leu Ser Pro Thr Gly Thr Arg Leu Ala Ser Thr Phe Val  
1100 1105 1110

Ser Glu Met Ser Ser Leu Leu Glu Met Leu Leu Glu Gln Arg Ser  
1115 1120 1125

Ser Met Pro Val Glu Ala Ala Ser Glu Ala Leu Arg Arg Leu Ser  
1130 1135 1140

Val Cys Gly Arg Thr Leu Ser Leu Asp Leu Ala Thr Ser Ala Ala  
1145 1150 1155

Ser Gly Met Lys Val Gln Gly Asp Pro Gly Gly Lys Thr Gly Thr  
1160 1165 1170

Glu Gly Lys Ser Arg Gly Ser Ser Ser Ser Ser Arg Cys Leu  
1175 1180

<210> 426

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 426

gtaagcacat gcctccagag gtgc 24

<210> 427

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 427

gtgacgtgga tgcttgggat gttg 24

<210> 428

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 428

tgacacctt cagtattgat gccagacag gccaggtcat tctgcgcga 50

<210> 429

<211> 2037

<212> DNA

<213> Homo sapiens

<400> 429

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cctgggagaa ggcagaccgt gtgagggggc ctgtggcccc agcgtgctgt 100

ggcctcgggg agtgggaagt ggaggcagga gccttcctta cacttcgcca 150

tgagtttctt catcgactcc agcatcatga ttacctcca gatactattt 200

tttgatttg ggtggctttt ctcatgcgc caattgtta aagactatga 250

gatacgtcag tatgtgtac aggtgatctt ctccgtgacg ttgcatttt 300

cttgaccat gtttgagctc atcatctttg aaatcttagg agtattgaat 350

agcagctccc gttattttca ctggaaaatg aacctgtgtg taattctgct 400

gatcctgggt ttcatgggtc cttttacat tggctatttt attgtgagca 450

atatccgact actgcataaa caacgactgc tttttcctg tctcttatgg 500

ctgaccttta tgtatttctt ctggaaacta ggagatccct ttccattct 550

cagcccaaaa catgggatct tatccataga acagctcatc agccgggttg 600

gtgtgattgg agtgactctc atggctcttc tttctggatt tggctctgtc 650

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ccaaacacgt aggatttccg tttaagggt cacatggaaa aggttatagc 1900

tttgcttga gattgactca ttaaaatcag agactgtaac aaaaaaaaaa 1950

aaaaaaaaa agggcggccg cgactctaga gtcgacctgc agaagcttgg 2000

ccgccatggc ccaacttgt tattgcagct tataatg 2037

<210> 430

<211> 455

<212> PRT

<213> Homo sapiens

<400> 430

Met Ser Phe Leu Ile Asp Ser Ser Ile Met Ile Thr Ser Gln Ile

1 5 10 15

Leu Phe Phe Gly Phe Gly Trp Leu Phe Phe Met Arg Gln Leu Phe

20 25 30

Lys Asp Tyr Glu Ile Arg Gln Tyr Val Val Gln Val Ile Phe Ser

35 40 45

Val Thr Phe Ala Phe Ser Cys Thr Met Phe Glu Leu Ile Ile Phe

50 55 60

Glu Ile Leu Gly Val Leu Asn Ser Ser Ser Arg Tyr Phe His Trp

65 70 75

Lys Met Asn Leu Cys Val Ile Leu Leu Ile Leu Val Phe Met Val

80 85 90

Pro Phe Tyr Ile Gly Tyr Phe Ile Val Ser Asn Ile Arg Leu Leu

95 100 105

His Lys Gln Arg Leu Leu Phe Ser Cys Leu Leu Trp Leu Thr Phe

110 115 120

Met Tyr Phe Phe Trp Lys Leu Gly Asp Pro Phe Pro Ile Leu Ser

125 130 135

Pro Lys His Gly Ile Leu Ser Ile Glu Gln Leu Ile Ser Arg Val

140 145 150

Gly Val Ile Gly Val Thr Leu Met Ala Leu Leu Ser Gly Phe Gly  
155 160 165

Ala Val Asn Cys Pro Tyr Thr Tyr Met Ser Tyr Phe Leu Arg Asn  
170 175 180

Val Thr Asp Thr Asp Ile Leu Ala Leu Glu Arg Arg Leu Leu Gln  
185 190 195

Thr Met Asp Met Ile Ile Ser Lys Lys Lys Arg Met Ala Met Ala  
200 205 210

Arg Arg Thr Met Phe Gln Lys Gly Glu Val His Asn Lys Pro Ser  
215 220 225

Gly Phe Trp Gly Met Ile Lys Ser Val Thr Thr Ser Ala Ser Gly  
230 235 240

Ser Glu Asn Leu Thr Leu Ile Gln Gln Glu Val Asp Ala Leu Glu  
245 250 255

Glu Leu Ser Arg Gln Leu Phe Leu Glu Thr Ala Asp Leu Tyr Ala  
260 265 270

Thr Lys Glu Arg Ile Glu Tyr Ser Lys Thr Phe Lys Gly Lys Tyr  
275 280 285

Phe Asn Phe Leu Gly Tyr Phe Phe Ser Ile Tyr Cys Val Trp Lys  
290 295 300

Ile Phe Met Ala Thr Ile Asn Ile Val Phe Asp Arg Val Gly Lys  
305 310 315

Thr Asp Pro Val Thr Arg Gly Ile Glu Ile Thr Val Asn Tyr Leu  
320 325 330

Gly Ile Gln Phe Asp Val Lys Phe Trp Ser Gln His Ile Ser Phe  
335 340 345

Ile Leu Val Gly Ile Ile Ile Val Thr Ser Ile Arg Gly Leu Leu  
350 355 360

Ile Thr Leu Thr Lys Phe Phe Tyr Ala Ile Ser Ser Ser Lys Ser  
365 370 375



Ser Asn Val Ile Val Leu Leu Leu Ala Gln Ile Met Gly Met Tyr  
380 385 390

Phe Val Ser Ser Val Leu Leu Ile Arg Met Ser Met Pro Leu Glu  
395 400 405

Tyr Arg Thr Ile Ile Thr Glu Val Leu Gly Glu Leu Gln Phe Asn  
410 415 420

Phe Tyr His Arg Trp Phe Asp Val Ile Phe Leu Val Ser Ala Leu  
425 430 435

Ser Ser Ile Leu Phe Leu Tyr Leu Ala His Lys Gln Ala Pro Glu  
440 445 450

Lys Gln Met Ala Pro  
455

<210> 431

<211> 407

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 78, 81, 113, 157, 224, 297

<223> unknown base

<400> 431

catgggaagt ggagccggag ccttccttac actcgccatg agtttctca 50

tcgactccag catcatgatt acctccnga nactattttt tggattggg 100

tggcttttct tcngcgccaa tgtttaaaga ctatgagata cgtcagtatg 150

ttgtacnggt gatcttctcc gtgacgttg ccatttcttg caccatgtt 200

gagctcatca tctttgaaat ctnggagta ttgaatagca gctcccgta 250

tttctactgg aaaatgaacc tgtgtgtaat tctgctgac ctggtntca 300

tggcgctttt ttacattggc tattttattg tgagcaatat ccgactactg 350

cataaacaac gactgctttt ttctgtctc ttatggctga cctttatga 400

ttccag 407

<210> 432

<211> 457

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 31, 66, 81-82, 84, 122, 184, 187, 232, 241, 400, 424, 427, 434

<223> unknown base

<400> 432

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gccaagggtt tcttnttga attccgggtt nngnatacct tccagaaaa 100

tatttttgg attggggta gnttttttc atgcgccaat tgttaaaga 150

ctatgagata cgtcagtatg ttgtacaggt gatntntcc gtgacgttg 200

cattttcttg caccatgttt gagctcatca tnttgaaat ntaggagta 250

ttgaatagca gctcccgta tttcactgg aaaatgaacc tgtgtgtaat 300

tctgctgac ctggtttca tggcgcttt ttacattggc tattttattg 350

tgagcaatat ccgactactg cataaacaac gactgctttt ttctgtctn 400

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cattctc 457

<210> 433

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 433

aagtggagcc ggagccttc 20

<210> 434

<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 434  
tcgttgttta tgcagtagtc gg 22

<210> 435  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 435  
attgtttaa gactatgaga tacgtcagta tgtgtacag g 41

<210> 436  
<211> 3951  
<212> DNA  
<213> Homo sapiens

<400> 436  
ctcgcgcagg gatcgtccca tggccggggc tcggagccgc gacccttggg 50  
  
gggcctccgg gatttgctac cttttggct cctgctcgt cgaactgctc 100  
  
ttctcacggg ctgtgcctt caatctggac gtgatgggtg ccttgcgcaa 150  
  
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gagctgatat gcaaaaggaa agcaaggaga accagtgggtt gggagtcagt 400  
  
gttcggagcc aggggcctgg gggcaagatt gttacctgtg cacaccgata 450

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ttcgtctatt tattaaaaaa tatttgagaa caaaaaaaaa aaaaaaaaaa 3950

a 3951

<210> 437

<211> 1141

<212> PRT

<213> Homo sapiens

<400> 437

Met Ala Gly Ala Arg Ser Arg Asp Pro Trp Gly Ala Ser Gly Ile

1 5 10 15

Cys Tyr Leu Phe Gly Ser Leu Leu Val Glu Leu Leu Phe Ser Arg

20 25 30

Ala Val Ala Phe Asn Leu Asp Val Met Gly Ala Leu Arg Lys Glu

35 40 45

Gly Glu Pro Gly Ser Leu Phe Gly Phe Ser Val Ala Leu His Arg

50 55 60

Gln Leu Gln Pro Arg Pro Gln Ser Trp Leu Leu Val Gly Ala Pro

65 70 75

Gln Ala Leu Ala Leu Pro Gly Gln Gln Ala Asn Arg Thr Gly Gly

80 85 90

Leu Phe Ala Cys Pro Leu Ser Leu Glu Glu Thr Asp Cys Tyr Arg

95 100 105

Val Asp Ile Asp Gln Gly Ala Asp Met Gln Lys Glu Ser Lys Glu

110 115 120

Asn Gln Trp Leu Gly Val Ser Val Arg Ser Gln Gly Pro Gly Gly

125 130 135

Lys Ile Val Thr Cys Ala His Arg Tyr Glu Ala Arg Gln Arg Val

140 145 150

Asp Gln Ile Leu Glu Thr Arg Asp Met Ile Gly Arg Cys Phe Val

155 160 165

Leu Ser Gln Asp Leu Ala Ile Arg Asp Glu Leu Asp Gly Gly Glu

170 175 180

Trp Lys Phe Cys Glu Gly Arg Pro Gln Gly His Glu Gln Phe Gly  
185 190 195

Phe Cys Gln Gln Gly Thr Ala Ala Ala Phe Ser Pro Asp Ser His  
200 205 210

Tyr Leu Leu Phe Gly Ala Pro Gly Thr Tyr Asn Trp Lys Gly Thr  
215 220 225

Ala Arg Val Glu Leu Cys Ala Gln Gly Ser Ala Asp Leu Ala His  
230 235 240

Leu Asp Asp Gly Pro Tyr Glu Ala Gly Gly Glu Lys Glu Gln Asp  
245 250 255

Pro Arg Leu Ile Pro Val Pro Ala Asn Ser Tyr Phe Gly Phe Ser  
260 265 270

Ile Asp Ser Gly Lys Gly Leu Val Arg Ala Glu Glu Leu Ser Phe  
275 280 285

Val Ala Gly Ala Pro Arg Ala Asn His Lys Gly Ala Val Val Ile  
290 295 300

Leu Arg Lys Asp Ser Ala Ser Arg Leu Val Pro Glu Val Met Leu  
305 310 315

Ser Gly Glu Arg Leu Thr Ser Gly Phe Gly Tyr Ser Leu Ala Val  
320 325 330

Ala Asp Leu Asn Ser Asp Gly Trp Pro Asp Leu Ile Val Gly Ala  
335 340 345

Pro Tyr Phe Phe Glu Arg Gln Glu Glu Leu Gly Gly Ala Val Tyr  
350 355 360

Val Tyr Leu Asn Gln Gly Gly His Trp Ala Gly Ile Ser Pro Leu  
365 370 375

Arg Leu Cys Gly Ser Pro Asp Ser Met Phe Gly Ile Ser Leu Ala  
380 385 390

Val Leu Gly Asp Leu Asn Gln Asp Gly Phe Pro Asp Ile Ala Val  
395 400 405



Gly Ala Pro Phe Asp Gly Asp Gly Lys Val Phe Ile Tyr His Gly  
410 415 420

Ser Ser Leu Gly Val Val Ala Lys Pro Ser Gln Val Leu Glu Gly  
425 430 435

Glu Ala Val Gly Ile Lys Ser Phe Gly Tyr Ser Leu Ser Gly Ser  
440 445 450

Leu Asp Met Asp Gly Asn Gln Tyr Pro Asp Leu Leu Val Gly Ser  
455 460 465

Leu Ala Asp Thr Ala Val Leu Phe Arg Ala Arg Pro Ile Leu His  
470 475 480

Val Ser His Glu Val Ser Ile Ala Pro Arg Ser Ile Asp Leu Glu  
485 490 495

Gln Pro Asn Cys Ala Gly Gly His Ser Val Cys Val Asp Leu Arg  
500 505 510

Val Cys Phe Ser Tyr Ile Ala Val Pro Ser Ser Tyr Ser Pro Thr  
515 520 525

Val Ala Leu Asp Tyr Val Leu Asp Ala Asp Thr Asp Arg Arg Leu  
530 535 540

Arg Gly Gln Val Pro Arg Val Thr Phe Leu Ser Arg Asn Leu Glu  
545 550 555

Glu Pro Lys His Gln Ala Ser Gly Thr Val Trp Leu Lys His Gln  
560 565 570

His Asp Arg Val Cys Gly Asp Ala Met Phe Gln Leu Gln Glu Asn  
575 580 585

Val Lys Asp Lys Leu Arg Ala Ile Val Val Thr Leu Ser Tyr Ser  
590 595 600

Leu Gln Thr Pro Arg Leu Arg Arg Gln Ala Pro Gly Gln Gly Leu  
605 610 615

Pro Pro Val Ala Pro Ile Leu Asn Ala His Gln Pro Ser Thr Gln  
620 625 630

Arg Ala Glu Ile His Phe Leu Lys Gln Gly Cys Gly Glu Asp Lys  
635 640 645

Ile Cys Gln Ser Asn Leu Gln Leu Val His Ala Arg Phe Cys Thr  
650 655 660

Arg Val Ser Asp Thr Glu Phe Gln Pro Leu Pro Met Asp Val Asp  
665 670 675

Gly Thr Thr Ala Leu Phe Ala Leu Ser Gly Gln Pro Val Ile Gly  
680 685 690

Leu Glu Leu Met Val Thr Asn Leu Pro Ser Asp Pro Ala Gln Pro  
695 700 705

Gln Ala Asp Gly Asp Asp Ala His Glu Ala Gln Leu Leu Val Met  
710 715 720

Leu Pro Asp Ser Leu His Tyr Ser Gly Val Arg Ala Leu Asp Pro  
725 730 735

Ala Glu Lys Pro Leu Cys Leu Ser Asn Glu Asn Ala Ser His Val  
740 745 750

Glu Cys Glu Leu Gly Asn Pro Met Lys Arg Gly Ala Gln Val Thr  
755 760 765

Phe Tyr Leu Ile Leu Ser Thr Ser Gly Ile Ser Ile Glu Thr Thr  
770 775 780

Glu Leu Glu Val Glu Leu Leu Leu Ala Thr Ile Ser Glu Gln Glu  
785 790 795

Leu His Pro Val Ser Ala Arg Ala Arg Val Phe Ile Glu Leu Pro  
800 805 810

Leu Ser Ile Ala Gly Met Ala Ile Pro Gln Gln Leu Phe Phe Ser  
815 820 825

Gly Val Val Arg Gly Glu Arg Ala Met Gln Ser Glu Arg Asp Val  
830 835 840

Gly Ser Lys Val Lys Tyr Glu Val Thr Val Ser Asn Gln Gly Gln  
845 850 855

Ser Leu Arg Thr Leu Gly Ser Ala Phe Leu Asn Ile Met Trp Pro  
860 865 870

His Glu Ile Ala Asn Gly Lys Trp Leu Leu Tyr Pro Met Gln Val  
875 880 885

Glu Leu Glu Gly Gly Gln Gly Pro Gly Gln Lys Gly Leu Cys Ser  
890 895 900

Pro Arg Pro Asn Ile Leu His Leu Asp Val Asp Ser Arg Asp Arg  
905 910 915

Arg Arg Arg Glu Leu Glu Pro Pro Glu Gln Gln Glu Pro Gly Glu  
920 925 930

Arg Gln Glu Pro Ser Met Ser Trp Trp Pro Val Ser Ser Ala Glu  
935 940 945

Lys Lys Lys Asn Ile Thr Leu Asp Cys Ala Arg Gly Thr Ala Asn  
950 955 960

Cys Val Val Phe Ser Cys Pro Leu Tyr Ser Phe Asp Arg Ala Ala  
965 970 975

Val Leu His Val Trp Gly Arg Leu Trp Asn Ser Thr Phe Leu Glu  
980 985 990

Glu Tyr Ser Ala Val Lys Ser Leu Glu Val Ile Val Arg Ala Asn  
995 1000 1005

Ile Thr Val Lys Ser Ser Ile Lys Asn Leu Met Leu Arg Asp Ala  
1010 1015 1020

Ser Thr Val Ile Pro Val Met Val Tyr Leu Asp Pro Met Ala Val  
1025 1030 1035

Val Ala Glu Gly Val Pro Trp Trp Val Ile Leu Leu Ala Val Leu  
1040 1045 1050

Ala Gly Leu Leu Val Leu Ala Leu Leu Val Leu Leu Trp Lys  
1055 1060 1065

Met Gly Phe Phe Lys Arg Ala Lys His Pro Glu Ala Thr Val Pro  
1070 1075 1080

Gln Tyr His Ala Val Lys Ile Pro Arg Glu Asp Arg Gln Gln Phe  
1085 1090 1095

Lys Glu Glu Lys Thr Gly Thr Ile Leu Arg Asn Asn Trp Gly Ser  
1100 1105 1110

Pro Arg Arg Glu Gly Pro Asp Ala His Pro Ile Leu Ala Ala Asp  
1115 1120 1125

Gly His Pro Glu Leu Gly Pro Asp Gly His Pro Gly Pro Gly Thr  
1130 1135 1140

Ala

<210> 438

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 438

ggctgacacc gcagtgtctt tcag 24

<210> 439

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 439

gctgtgtggg actgcaatgt agct 24

<210> 440

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 440

catcctccat gtctcccatg aggtctctat tgctccacga agcatc 46

<210> 441

<211> 1964

<212> DNA

<213> Homo sapiens

<400> 441

cgcgccgggc gcaggagct gaggggacgg ctgagacgg cggcgcgtgc 50

agcagctcca gaaagcagcg agttggcaga gcagggtgc attccagca 100

ggagctgcga gcacagtgtt ggctcacaac aagatgtca aggtgtcagc 150

cgtactgtgt gtgtgtgcag ccgcttggtg cagtcagtct ctgcagctg 200

ccgcggcggg ggctgcagcc ggggggcggg cggacggcgg taattttctg 250

gatgataaac aatggctcac cacaatctct cagtatgaca aggaagtcgg 300

acagtggaac aaattccgag acgaagtaga ggatgattat ttccgcactt 350

ggagtccagg aaaacccttc gacaggctt tagatccagc taaggatcca 400

tgcttaaaga tgaatgtag tcgccataaa gtagcattg ctcaagattc 450

tcagactgca gtctgcatta gtcaccggag gcttacacac aggatgaaag 500

aagcaggagt agaccatagg cagtgaggagg gtcccatatt atccacctgc 550

aagcagtgcc cagtggtcta tccagccct gttgtggtt cagatgtca 600

tacctactct ttccagtgc aactagaata tcaggcatgt gtcttaggaa 650

aacagatctc agtcaaatgt gaaggacatt gccatgtcc ttacagataag 700

cccaccagta caagcagaaa tgtaagaga gcatgcagtg acctggagtt 750

cagggaagtg gcaaacagat tgcgggactg gttcaaggcc ctcatgaaa 800

gtggaagtca aaacaagaag acaaaaacat tgctgaggcc tgagagaagc 850

agattcgata ccagcatctt gccaatgtc aaggactcac ttggtggat 900

gtttaacaga cttgatacaa actatgacct gctattggac cagtcagagc 950  
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aattcttgtg acacatacaa ggacagtta atatctaata atgagtgggtg 1050  
ctactgcttc cagagacagc aagaccacc ttgccagact gagtcagca 1100  
atattcagaa gcggcaaggg gtaaagaagc tcctaggaca gtatatcccc 1150  
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tggacagtgc tgggtgttg acagatatgg aatgaagtc atgggatcca 1250  
gaataaatgg tgttcagat tgtgctatag attttgagat ctccggagat 1300  
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gggatgatga tgatgggtgt gatgaccatg atgtatacat ttgattgatg 1450  
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cctatttaaa attatcttct tcccaataa caaatgatt ctaaacctca 1550  
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caaatgaca gctagtgtt gggatcgtac atgttaattt ttgaaagat 1800  
aattctaagt gaaatttaaa ataaataaat ttttaatgac ctgggtctta 1850  
aggatttagg aaaaatatgc atgctttaat tgcatctca aagtagcatc 1900  
ttgctagacc tagatgagtc aggataacag agagatacca catgactcca 1950  
aaaaaaaaaa aaaa 1964

<211> 436

<212> PRT

<213> Homo sapiens

<400> 442

Met Leu Lys Val Ser Ala Val Leu Cys Val Cys Ala Ala Ala Trp

1 5 10 15

Cys Ser Gln Ser Leu Ala Ala Ala Ala Val Ala Ala Ala Gly

20 25 30

Gly Arg Ser Asp Gly Gly Asn Phe Leu Asp Asp Lys Gln Trp Leu

35 40 45

Thr Thr Ile Ser Gln Tyr Asp Lys Glu Val Gly Gln Trp Asn Lys

50 55 60

Phe Arg Asp Glu Val Glu Asp Asp Tyr Phe Arg Thr Trp Ser Pro

65 70 75

Gly Lys Pro Phe Asp Gln Ala Leu Asp Pro Ala Lys Asp Pro Cys

80 85 90

Leu Lys Met Lys Cys Ser Arg His Lys Val Cys Ile Ala Gln Asp

95 100 105

Ser Gln Thr Ala Val Cys Ile Ser His Arg Arg Leu Thr His Arg

110 115 120

Met Lys Glu Ala Gly Val Asp His Arg Gln Trp Arg Gly Pro Ile

125 130 135

Leu Ser Thr Cys Lys Gln Cys Pro Val Val Tyr Pro Ser Pro Val

140 145 150

Cys Gly Ser Asp Gly His Thr Tyr Ser Phe Gln Cys Lys Leu Glu

155 160 165

Tyr Gln Ala Cys Val Leu Gly Lys Gln Ile Ser Val Lys Cys Glu

170 175 180

Gly His Cys Pro Cys Pro Ser Asp Lys Pro Thr Ser Thr Ser Arg

185 190 195

Asn Val Lys Arg Ala Cys Ser Asp Leu Glu Phe Arg Glu Val Ala

200	205	210
Asn Arg Leu Arg Asp Trp Phe Lys Ala Leu His Glu Ser Gly Ser		
215	220	225
Gln Asn Lys Lys Thr Lys Thr Leu Leu Arg Pro Glu Arg Ser Arg		
230	235	240
Phe Asp Thr Ser Ile Leu Pro Ile Cys Lys Asp Ser Leu Gly Trp		
245	250	255
Met Phe Asn Arg Leu Asp Thr Asn Tyr Asp Leu Leu Leu Asp Gln		
260	265	270
Ser Glu Leu Arg Ser Ile Tyr Leu Asp Lys Asn Glu Gln Cys Thr		
275	280	285
Lys Ala Phe Phe Asn Ser Cys Asp Thr Tyr Lys Asp Ser Leu Ile		
290	295	300
Ser Asn Asn Glu Trp Cys Tyr Cys Phe Gln Arg Gln Gln Asp Pro		
305	310	315
Pro Cys Gln Thr Glu Leu Ser Asn Ile Gln Lys Arg Gln Gly Val		
320	325	330
Lys Lys Leu Leu Gly Gln Tyr Ile Pro Leu Cys Asp Glu Asp Gly		
335	340	345
Tyr Tyr Lys Pro Thr Gln Cys His Gly Ser Val Gly Gln Cys Trp		
350	355	360
Cys Val Asp Arg Tyr Gly Asn Glu Val Met Gly Ser Arg Ile Asn		
365	370	375
Gly Val Ala Asp Cys Ala Ile Asp Phe Glu Ile Ser Gly Asp Phe		
380	385	390
Ala Ser Gly Asp Phe His Glu Trp Thr Asp Asp Glu Asp Asp Glu		
395	400	405
Asp Asp Ile Met Asn Asp Glu Asp Glu Ile Glu Asp Asp Asp Glu		
410	415	420
Asp Glu Gly Asp Asp Asp Asp Gly Gly Asp Asp His Asp Val Tyr		



425

430

435

Ile

<210> 443

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 443

cagcaatatt cagaagcggc aaggg 25

<210> 444

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 444

catcatggtc atcaccacca tcatcatc 28

<210> 445

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 445

ggttactaca agccaacaca atgtcatggc agtgttggac agtgctgg 48

<210> 446

<211> 3617

<212> DNA

<213> Homo sapiens

<400> 446

cagactccag atttcctgt caaccacgag gagtccagag aggaaacgcg 50

gagcggagac aacagtacct gacgcctctt tcagcccggg atgccccag 100  
cagggatggg cgacaagatc tggctgccct tccccgtgct cttctggcc 150  
gctctgctc cgggtgctgt gcctggggcg gccgggttca caccttcct 200  
cgatagcgac ttcaccttta ccttcccg cggccagaag gaggcttct 250  
accagcccat gccctgaag gcctcgctgg agatcgagta ccaagttta 300  
gatggagcag gattagatat tgattccat ctgcctctc cagaaggca 350  
aaccttagtt ttgaacaaa gaaaatcaga tggagttcac actgtagaga 400  
ctgaagtgg tgattacatg ttctgcttg acaatacatt cagcaccatt 450  
tctgagaagg tgatttctt tgaattaatc ctggataata tgggagaaca 500  
ggcacaagaa caagaagatt ggaagaaata tattactggc acagatatat 550  
tggatatgaa actggaagac atcctggaat ccatcaacag catcaagtcc 600  
agactaagca aaagtgggca catacaaatt ctgcttagag cattgaagc 650  
tcgtgatcga aacatacaag aaagcaactt tgatagagtc aatttctgt 700  
ctatggttaa ttagtggtc atggtggtg tgcagccat tcaagttat 750  
atgctgaaga gtctgttga agataagagg aaaagtagaa cttaaaactc 800  
caaactagag tacgtaacat tgaaaaatga ggcataaaaa tgcaataaac 850  
tgttacagtc aagaccatta atggtcttct ccaaaatatt ttgagatata 900  
aaagtaggaa acaggtataa tttaatgtg aaaattaagt cttcacttc 950  
tgtgcaagta atcctgctga tccagttga cttaagtgtg taacaggaat 1000  
atttgcaga atataggttt aactgaatga agccatatta ataactgcat 1050  
tttctaact ttgaaaaatt ttgcaaatgt cttagtgat ttaaataaat 1100  
gagtattggg cctaattgca acaccagtct gttttaaca ggttctatta 1150  
cccagaactt tttgtaaat gcggcagtta caaattaact gtggaagttt 1200

tcagttttaa gttataaat acctgagaat tacctaatga tggattgaat 1250  
aaatcttttag actacaaaag cccaactttt ctctatttac atatgcatct 1300  
ctcctataat gtaaatagaa taatagcttt gaaatacaat taggttttg 1350  
agatttttat aaccaataac atttcagtgt aacatattag cagaaagcat 1400  
tagtctttgt actttgctta cattcccaa agctgacatt ttcacgattc 1450  
ttaaaaacac aaagttacac ttactaaaat taggacatgt ttctctttg 1500  
aatgaagaa tatagtttaa aagcttcctc ctccataggg acacatttc 1550  
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taaataaata tctccttttc tgagctctaa gaattatcag aaaacaggaa 1800  
agaatttaga aaaacttgag aaaaccta ccaaataaa attcacttaa 1850  
gtagaactat aaataaatat ctagaatctg actggctcat catgacatcc 1900  
tactcataac ataaatcaaa ggagatgatt aattccagt tagctggaag 1950  
aaactttggc ttaggtttt tattttctac aagaattctg gtttgaatta 2000  
ttttgtaag caggtacatt ttataaatg taagccctac tgtaaggttt 2050  
agcactgggt gtacatat tttaaaaatt ttattataa caactttat 2100  
taaatggcc ttctgaaca ctttattat tgatgtgaa gtaaggatta 2150  
gaaacataga ctccaagti ttaaacacct aaatgtgaat aacctatata 2200  
tacaacaaag ttctgccat ctagctttt gaagtctatg ggggtcttac 2250  
tcaagtacta gtaatttaac ttcatcatga atgaactata attttaagt 2300  
tatgcccat tataacgttg ttatgacta cattgtgagt tagaaacaaa 2350

cttaaaattt ggggtataga acccctcaac aggttagtaa tgctggaatt 2400  
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tagtataaaa agagatacat ttccctctta ggcccctggg agaagagcag 2500  
cttagatttc cctactggca aggtttttaa aaatgaggta aatgccgtat 2550  
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acatgtatga tttgtgccac tgactctaaa cctatgattc agtaacttct 2900  
taccatataa aaacgataat tgctttattt ggaaaagaat ttaggaatac 2950  
taaggacaat tattttata gacaaagtaa aaagacagat atttaagagg 3000  
cataaccaa aaagcaaac ttgtaaacag agtaaaaatc ttaatatatt 3050  
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tccatttcta aattaaagt atgctaaatt gagtaagctg ttatcactt 3150  
aacagctcat tttgtcttt tcaatatata aattttaaaa atactacaat 3200  
atttaactaa ggcccaaccg atttcataa tgtagcagtt accgtgttca 3250  
cctcacacta aggcctagag tttgctctga tatgcattg gatgattaat 3300  
gttatgctgt tctttcatgt gaatgtcaag acatggaggg tgtttgtaat 3350  
tttatggtaa aattaatcct tcttacacat aatggtgtct taaaattgac 3400  
aaaaaatgag cacttacaat tgtatgtct ctaaatgaa gattctttat 3450  
gtgaaatttt aaaagacatt gattccgcat gtaaggattt tcatctgaa 3500

gtacaataat gcacaatcag tgttgctcaa actgctttat acttataaac 3550

agccatctta aataagcaac gtattgtgag tactgatatg tatataataa 3600

aaattatcaa aggaaaa 3617

<210> 447

<211> 229

<212> PRT

<213> Homo sapiens

<400> 447

Met Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Leu Ala

1 5 10 15

Ala Leu Pro Pro Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro

20 25 30

Ser Leu Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys

35 40 45

Glu Cys Phe Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile

50 55 60

Glu Tyr Gln Val Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His

65 70 75

Leu Ala Ser Pro Glu Gly Lys Thr Leu Val Phe Glu Gln Arg Lys

80 85 90

Ser Asp Gly Val His Thr Val Glu Thr Glu Val Gly Asp Tyr Met

95 100 105

Phe Cys Phe Asp Asn Thr Phe Ser Thr Ile Ser Glu Lys Val Ile

110 115 120

Phe Phe Glu Leu Ile Leu Asp Asn Met Gly Glu Gln Ala Gln Glu

125 130 135

Gln Glu Asp Trp Lys Lys Tyr Ile Thr Gly Thr Asp Ile Leu Asp

140 145 150

Met Lys Leu Glu Asp Ile Leu Glu Ser Ile Asn Ser Ile Lys Ser

155 160 165

Arg Leu Ser Lys Ser Gly His Ile Gln Ile Leu Leu Arg Ala Phe  
170 175 180

Glu Ala Arg Asp Arg Asn Ile Gln Glu Ser Asn Phe Asp Arg Val  
185 190 195

Asn Phe Trp Ser Met Val Asn Leu Val Val Met Val Val Val Ser  
200 205 210

Ala Ile Gln Val Tyr Met Leu Lys Ser Leu Phe Glu Asp Lys Arg  
215 220 225

Lys Ser Arg Thr

<210> 448

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 448

cccagcaggg ctgggcgaca aga 23

<210> 449

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 449

gtcttcagtt ttcatatcca ata 23

<210> 450

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 450

ccagaaggag cacggggaag ggcagccaga tctgtcgcc cat 43

<210> 451

<211> 859

<212> DNA

<213> Homo sapiens

<400> 451

ccatccctga gatcttttta taaaaaaccc agtctttgct gaccagacaa 50

agcataccag atctcaccag agatgcgag acactatgct gcctcccatg 100

gccctgccc gtgtgtcctg gatgctgctt tctgcctca ttctcctgtg 150

tcaggttaa ggtgaagaaa cccagaagga actgccctct ccacggatca 200

gctgtcccaa aggtccaag gcctatggct cccctgcta tgccttggtt 250

ttgtaccaa aatcctggat ggatgcagat ctggcttgcc agaagcggcc 300

ctctggaaaa ctggtgtctg tgctcagtgg ggctgaggga tccttcgtgt 350

cctccctggt gaggagcatt agtaacagct actcatacat ctggattggg 400

ctccatgacc ccacacaggg ctctgagcct gatggagatg gatgggagtg 450

gagtagcact gatgtgatga attactttgc atgggagaaa aatccctcca 500

ccatcttaaa ccctggccac tgtgggagcc tgtcaagaag cacaggattt 550

ctgaagtga aagattataa ctgtgatgca aagttaccct atgtctgcaa 600

gttcaaggac tagggcaggt gggaagtcag cagcctcagc ttggcgtgca 650

gctcatcatg gacatgagac cagtgtgaag actcaccctg gaagagaata 700

tttccccaa actgccctac ctgactacct tgtcatgac ctccttcttt 750

ttccttttc ttcaccttca ttcaggctt ttctctgtct tccatgtctt 800

gagatctcag agaataataa taaaaatgtt actttataaa aaaaaaaaaa 850

aaaaaaaaa 859

<210> 452  
<211> 175  
<212> PRT  
<213> Homo sapiens

<400> 452  
Met Leu Pro Pro Met Ala Leu Pro Ser Val Ser Trp Met Leu Leu  
1 5 10 15  
Ser Cys Leu Ile Leu Leu Cys Gln Val Gln Gly Glu Glu Thr Gln  
20 25 30  
Lys Glu Leu Pro Ser Pro Arg Ile Ser Cys Pro Lys Gly Ser Lys  
35 40 45  
Ala Tyr Gly Ser Pro Cys Tyr Ala Leu Phe Leu Ser Pro Lys Ser  
50 55 60  
Trp Met Asp Ala Asp Leu Ala Cys Gln Lys Arg Pro Ser Gly Lys  
65 70 75  
Leu Val Ser Val Leu Ser Gly Ala Glu Gly Ser Phe Val Ser Ser  
80 85 90  
Leu Val Arg Ser Ile Ser Asn Ser Tyr Ser Tyr Ile Trp Ile Gly  
95 100 105  
Leu His Asp Pro Thr Gln Gly Ser Glu Pro Asp Gly Asp Gly Trp  
110 115 120  
Glu Trp Ser Ser Thr Asp Val Met Asn Tyr Phe Ala Trp Glu Lys  
125 130 135  
Asn Pro Ser Thr Ile Leu Asn Pro Gly His Cys Gly Ser Leu Ser  
140 145 150  
Arg Ser Thr Gly Phe Leu Lys Trp Lys Asp Tyr Asn Cys Asp Ala  
155 160 165  
Lys Leu Pro Tyr Val Cys Lys Phe Lys Asp  
170 175

<210> 453  
<211> 550  
<212> DNA



<213> Homo sapiens

<400> 453

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ggcgctcctg gcgtggtgc tggtgcctg cggagagctg gcgccggccc 150  
tgcgtgcta cgtctgtccg gagcccacag gagtgtcgga ctgtgtcacc 200  
atcgccacct gcaccaccaa cgaaacatg tgcaagacca cactctactc 250  
ccgggagata gtgtaccctt tccaggggga ctccacggtg accaagtctt 300  
gtgccagcaa gtgaagccc tcggatgtgg atggcatcgg ccagaccctg 350  
cccgtgtcct gctgcaatac tgagctgtgc aatgtagacg gggcgccccg 400  
tctgaacagc ctccactgcg gggccctcac gctcctccca ctcttgagcc 450  
tccgactgta gattccccgc ccaccccat ggccctatgc ggcccagccc 500  
cgaatgcctt gaagaagtgc cccctgcacc aggaaaaaaaa aaaaaaaaaa 550

<210> 454

<211> 125

<212> PRT

<213> Homo sapiens

<400> 454

Met Arg Gly Thr Arg Leu Ala Leu Leu Ala Leu Val Leu Ala Ala  
1 5 10 15  
Cys Gly Glu Leu Ala Pro Ala Leu Arg Cys Tyr Val Cys Pro Glu  
20 25 30  
Pro Thr Gly Val Ser Asp Cys Val Thr Ile Ala Thr Cys Thr Thr  
35 40 45  
Asn Glu Thr Met Cys Lys Thr Thr Leu Tyr Ser Arg Glu Ile Val  
50 55 60  
Tyr Pro Phe Gln Gly Asp Ser Thr Val Thr Lys Ser Cys Ala Ser  
65 70 75

Lys Cys Lys Pro Ser Asp Val Asp Gly Ile Gly Gln Thr Leu Pro  
80 85 90

Val Ser Cys Cys Asn Thr Glu Leu Cys Asn Val Asp Gly Ala Pro  
95 100 105

Ala Leu Asn Ser Leu His Cys Gly Ala Leu Thr Leu Leu Pro Leu  
110 115 120

Leu Ser Leu Arg Leu  
125

<210> 455

<211> 1518

<212> DNA

<213> Homo sapiens

<400> 455

ctgcagtcag gactctggga ccgcaggggg ctcccgacc ctgactctgc 50

agccgaaccg gcacggtttc gtggggaccc aggcttgcaa agtgacggtc 100

attttcttt tctttctccc tcttgagtc ttctgagatg atggctctgg 150

gcgcagcggg agctaccggg gtctttgtcg cgatggtagc ggcggtctc 200

ggcgccacc ctctgctggg agtgagcgcc acctgaact cggttctcaa 250

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accagggctc tgcagtcagc gccgcgccgg gaatcctgta cccgggcggg 350

aataagtacc agaccattga caactaccag ccgtaccgt gcgcagagga 400

cgaggagtgc ggcaactgat agtactgcgc tagtcccacc cgcggagggg 450

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tgtgtcttct gatcaaaatc atttccgagg agaaattgag gaaaccatca 600

ctgaaagctt tggtaatgat catagcacct tggatgggta ttccagaaga 650

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 <211> 266  
 <212> PRT  
 <213> Homo sapiens

<400> 456  
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Ala Thr Leu Asn Ser Val Leu Asn Ser Asn Ala Ile Lys Asn Leu  
35 40 45

Pro Pro Pro Leu Gly Gly Ala Ala Gly His Pro Gly Ser Ala Val  
50 55 60

Ser Ala Ala Pro Gly Ile Leu Tyr Pro Gly Gly Asn Lys Tyr Gln  
65 70 75

Thr Ile Asp Asn Tyr Gln Pro Tyr Pro Cys Ala Glu Asp Glu Glu  
80 85 90

Cys Gly Thr Asp Glu Tyr Cys Ala Ser Pro Thr Arg Gly Gly Asp  
95 100 105

Ala Gly Val Gln Ile Cys Leu Ala Cys Arg Lys Arg Arg Lys Arg  
110 115 120

Cys Met Arg His Ala Met Cys Cys Pro Gly Asn Tyr Cys Lys Asn  
125 130 135

Gly Ile Cys Val Ser Ser Asp Gln Asn His Phe Arg Gly Glu Ile  
140 145 150

Glu Glu Thr Ile Thr Glu Ser Phe Gly Asn Asp His Ser Thr Leu  
155 160 165

Asp Gly Tyr Ser Arg Arg Thr Thr Leu Ser Ser Lys Met Tyr His  
170 175 180

Thr Lys Gly Gln Glu Gly Ser Val Cys Leu Arg Ser Ser Asp Cys  
185 190 195

Ala Ser Gly Leu Cys Cys Ala Arg His Phe Trp Ser Lys Ile Cys  
200 205 210

Lys Pro Val Leu Lys Glu Gly Gln Val Cys Thr Lys His Arg Arg  
215 220 225

Lys Gly Ser His Gly Leu Glu Ile Phe Gln Arg Cys Tyr Cys Gly  
230 235 240

Glu Gly Leu Ser Cys Arg Ile Gln Lys Asp His His Gln Ala Ser  
245 250 255

Asn Ser Ser Arg Leu His Thr Cys Gln Arg His  
260 265

<210> 457

<211> 638

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 30, 123, 133, 139, 180, 214, 259, 282, 308, 452, 467, 471, 473,  
509, 556

<223> unknown base

<400> 457

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cattttttt tctttctct tcnngagtcc ttntgagang atggttttgg 150

gcgcagcggg agctaaccg gtttttgn gcgatggtag cggcggttt 200

cggcggccac ctntgctgg gagtgagcg caccttgaat cggttttcaa 250

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atgcgtcang ctatgtgctg ccccggaat tactgcaaaa atggaatatg 550

tgtgtnttct gatcaaaatc atttccgagg agaaattgag gaaaccatca 600

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<211> 4040

<212> DNA

<213> Homo sapiens

<400> 458

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<210> 459

<211> 747

<212> PRT

<213> Homo sapiens

<400> 459

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Gly Thr Asp Gln Asp Phe Tyr Ser Leu Leu Gly Val Ser Lys Thr

35 40 45

Ala Ser Ser Arg Glu Ile Arg Gln Ala Phe Lys Lys Leu Ala Leu

50 55 60

Lys Leu His Pro Asp Lys Asn Pro Asn Asn Pro Asn Ala His Gly

65	70	75
Asp Phe Leu Lys Ile Asn Arg Ala Tyr Glu Val Leu Lys Asp Glu		
80	85	90
Asp Leu Arg Lys Lys Tyr Asp Lys Tyr Gly Glu Lys Gly Leu Glu		
95	100	105
Asp Asn Gln Gly Gly Gln Tyr Glu Ser Trp Asn Tyr Tyr Arg Tyr		
110	115	120
Asp Phe Gly Ile Tyr Asp Asp Asp Pro Glu Ile Ile Thr Leu Glu		
125	130	135
Arg Arg Glu Phe Asp Ala Ala Val Asn Ser Gly Glu Leu Trp Phe		
140	145	150
Val Asn Phe Tyr Ser Pro Gly Cys Ser His Cys His Asp Leu Ala		
155	160	165
Pro Thr Trp Arg Asp Phe Ala Lys Glu Val Asp Gly Leu Leu Arg		
170	175	180
Ile Gly Ala Val Asn Cys Gly Asp Asp Arg Met Leu Cys Arg Met		
185	190	195
Lys Gly Val Asn Ser Tyr Pro Ser Leu Phe Ile Phe Arg Ser Gly		
200	205	210
Met Ala Pro Val Lys Tyr His Gly Asp Arg Ser Lys Glu Ser Leu		
215	220	225
Val Ser Phe Ala Met Gln His Val Arg Ser Thr Val Thr Glu Leu		
230	235	240
Trp Thr Gly Asn Phe Val Asn Ser Ile Gln Thr Ala Phe Ala Ala		
245	250	255
Gly Ile Gly Trp Leu Ile Thr Phe Cys Ser Lys Gly Gly Asp Cys		
260	265	270
Leu Thr Ser Gln Thr Arg Leu Arg Leu Ser Gly Met Leu Phe Leu		
275	280	285
Asn Ser Leu Asp Ala Lys Glu Ile Tyr Leu Glu Val Ile His Asn		

290	295	300
Leu Pro Asp Phe Glu Leu Leu Ser Ala Asn Thr Leu Glu Asp Arg		
305	310	315
Leu Ala His His Arg Trp Leu Leu Phe Phe His Phe Gly Lys Asn		
320	325	330
Glu Asn Ser Asn Asp Pro Glu Leu Lys Lys Leu Lys Thr Leu Leu		
335	340	345
Lys Asn Asp His Ile Gln Val Gly Arg Phe Asp Cys Ser Ser Ala		
350	355	360
Pro Asp Ile Cys Ser Asn Leu Tyr Val Phe Gln Pro Ser Leu Ala		
365	370	375
Val Phe Lys Gly Gln Gly Thr Lys Glu Tyr Glu Ile His His Gly		
380	385	390
Lys Lys Ile Leu Tyr Asp Ile Leu Ala Phe Ala Lys Glu Ser Val		
395	400	405
Asn Ser His Val Thr Thr Leu Gly Pro Gln Asn Phe Pro Ala Asn		
410	415	420
Asp Lys Glu Pro Trp Leu Val Asp Phe Phe Ala Pro Trp Cys Pro		
425	430	435
Pro Cys Arg Ala Leu Leu Pro Glu Leu Arg Arg Ala Ser Asn Leu		
440	445	450
Leu Tyr Gly Gln Leu Lys Phe Gly Thr Leu Asp Cys Thr Val His		
455	460	465
Glu Gly Leu Cys Asn Met Tyr Asn Ile Gln Ala Tyr Pro Thr Thr		
470	475	480
Val Val Phe Asn Gln Ser Asn Ile His Glu Tyr Glu Gly His His		
485	490	495
Ser Ala Glu Gln Ile Leu Glu Phe Ile Glu Asp Leu Met Asn Pro		
500	505	510
Ser Val Val Ser Leu Thr Pro Thr Thr Phe Asn Glu Leu Val Thr		

515	520	525
Gln Arg Lys His Asn Glu Val Trp Met Val Asp Phe Tyr Ser Pro		
530	535	540
Trp Cys His Pro Cys Gln Val Leu Met Pro Glu Trp Lys Arg Met		
545	550	555
Ala Arg Thr Leu Thr Gly Leu Ile Asn Val Gly Ser Ile Asp Cys		
560	565	570
Gln Gln Tyr His Ser Phe Cys Ala Gln Glu Asn Val Gln Arg Tyr		
575	580	585
Pro Glu Ile Arg Phe Phe Pro Pro Lys Ser Asn Lys Ala Tyr Gln		
590	595	600
Tyr His Ser Tyr Asn Gly Trp Asn Arg Asp Ala Tyr Ser Leu Arg		
605	610	615
Ile Trp Gly Leu Gly Phe Leu Pro Gln Val Ser Thr Asp Leu Thr		
620	625	630
Pro Gln Thr Phe Ser Glu Lys Val Leu Gln Gly Lys Asn His Trp		
635	640	645
Val Ile Asp Phe Tyr Ala Pro Trp Cys Gly Pro Cys Gln Asn Phe		
650	655	660
Ala Pro Glu Phe Glu Leu Leu Ala Arg Met Ile Lys Gly Lys Val		
665	670	675
Lys Ala Gly Lys Val Asp Cys Gln Ala Tyr Ala Gln Thr Cys Gln		
680	685	690
Lys Ala Gly Ile Arg Ala Tyr Pro Thr Val Lys Phe Tyr Phe Tyr		
695	700	705
Glu Arg Ala Lys Arg Asn Phe Gln Glu Glu Gln Ile Asn Thr Arg		
710	715	720
Asp Ala Lys Ala Ile Ala Ala Leu Ile Ser Glu Lys Leu Glu Thr		
725	730	735
Leu Arg Asn Gln Gly Lys Arg Asn Lys Asp Glu Leu		

740

745

<210> 460

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 460

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<210> 461

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 461

gatcagccag ccaataccag cagc 24

<210> 462

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 462

gtggtgatga tagaatgctt tgccgaatga aaggagtcaa cagctatccc 50

<210> 463

<211> 1818

<212> DNA

<213> Homo sapiens

<400> 463

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atggacccaa gagaagaa 1818

<210> 464

<211> 300

<212> PRT

<213> Homo sapiens

<400> 464

Met Asn Ile Ile Leu Glu Ile Leu Leu Leu Ile Thr Ile Ile

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Tyr Ser Tyr Leu Glu Ser Leu Val Lys Phe Phe Ile Pro Gln Arg

20 25 30

Arg Lys Ser Val Ala Gly Glu Ile Val Leu Ile Thr Gly Ala Gly

35 40 45

His Gly Ile Gly Arg Gln Thr Thr Tyr Glu Phe Ala Lys Arg Gln

50 55 60

Ser Ile Leu Val Leu Trp Asp Ile Asn Lys Arg Gly Val Glu Glu

65 70 75

Thr Ala Ala Glu Cys Arg Lys Leu Gly Val Thr Ala His Ala Tyr  
80 85 90

Val Val Asp Cys Ser Asn Arg Glu Glu Ile Tyr Arg Ser Leu Asn  
95 100 105

Gln Val Lys Lys Glu Val Gly Asp Val Thr Ile Val Val Asn Asn  
110 115 120

Ala Gly Thr Val Tyr Pro Ala Asp Leu Leu Ser Thr Lys Asp Glu  
125 130 135

Glu Ile Thr Lys Thr Phe Glu Val Asn Ile Leu Gly His Phe Trp  
140 145 150

Ile Thr Lys Ala Leu Leu Pro Ser Met Met Glu Arg Asn His Gly  
155 160 165

His Ile Val Thr Val Ala Ser Val Cys Gly His Glu Gly Ile Pro  
170 175 180

Tyr Leu Ile Pro Tyr Cys Ser Ser Lys Phe Ala Ala Val Gly Phe  
185 190 195

His Arg Gly Leu Thr Ser Glu Leu Gln Ala Leu Gly Lys Thr Gly  
200 205 210

Ile Lys Thr Ser Cys Leu Cys Pro Val Phe Val Asn Thr Gly Phe  
215 220 225

Thr Lys Asn Pro Ser Thr Arg Leu Trp Pro Val Leu Glu Thr Asp  
230 235 240

Glu Val Val Arg Ser Leu Ile Asp Gly Ile Leu Thr Asn Lys Lys  
245 250 255

Met Ile Phe Val Pro Ser Tyr Ile Asn Ile Phe Leu Arg Leu Gln  
260 265 270

Lys Phe Leu Pro Glu Arg Ala Ser Ala Ile Leu Asn Arg Met Gln  
275 280 285

Asn Ile Gln Phe Glu Ala Val Val Gly His Lys Ile Lys Met Lys  
290 295 300



<210> 465  
<211> 1547  
<212> DNA  
<213> Homo sapiens

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gcaccaactg gaagcgcgtg atgatcgtgc tgagcggaag cctgctgcac 700  
cgcggtgcgc cctaccgga cccgctgcgc atccgcgcg agcacgtgca 750  
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ctcttcgtgc gcgaccctt cgtgcgcctg atctccgct tccgcagcaa 900  
gttcgagctg gagaacgagg agttctaccg caagttcgcc gtgcccacgc 950  
tgcggtgta cgccaaccac accagcctgc ccgcctcggc gcgcgaggcc 1000

ttccgcgctg gcctcaaggt gtccttcgcc aacttcatcc agtacctgct 1050  
 ggacccgcac acggagaagc tggcgccctt caacgagcac tggcggcagg 1100  
 tgtaccgcct ctgccacccg tgccagatcg actacgactt cgtggggaag 1150  
 ctggagactc tggacgagga cgccgcgcag ctgctgcagc tactccaggt 1200  
 ggaccggcag ctccgcttcc ccccgagcta ccggaacagg accgccagca 1250  
 gctgggagga ggactgggtc gccaaagatcc cctggcctg gaggcagcag 1300  
 ctgtataaac tctacgaggc cgactttgtt ctcttcggct accccaagcc 1350  
 cgaaaacctc ctccgagact gaaagcttgc gcgttgcttt ttctcgcgtg 1400  
 cctggaacct gacgcacgcg cactccagtt ttttatgac ctacgatttt 1450  
 gcaatctggg cttcttggtc actccactgc ctctatccat tgagtactgt 1500  
 atcgatattg tttttaaga ttaatatatt tcaggtattt aatacga 1547

<210> 466

<211> 414

<212> PRT

<213> Homo sapiens

<400> 466

Met Thr Lys Ala Arg Leu Phe Arg Leu Trp Leu Val Leu Gly Ser  
 1 5 10 15

Val Phe Met Ile Leu Leu Ile Ile Val Tyr Trp Asp Ser Ala Gly  
 20 25 30

Ala Ala His Phe Tyr Leu His Thr Ser Phe Ser Arg Pro His Thr  
 35 40 45

Gly Pro Pro Leu Pro Thr Pro Gly Pro Asp Arg Asp Arg Glu Leu  
 50 55 60

Thr Ala Asp Ser Asp Val Asp Glu Phe Leu Asp Lys Phe Leu Ser  
 65 70 75

Ala Gly Val Lys Gln Ser Asp Leu Pro Arg Lys Glu Thr Glu Gln  
 80 85 90

Pro Pro Ala Pro Gly Ser Met Glu Glu Ser Val Arg Gly Tyr Asp  
95 100 105

Trp Ser Pro Arg Asp Ala Arg Arg Ser Pro Asp Gln Gly Arg Gln  
110 115 120

Gln Ala Glu Arg Arg Ser Val Leu Arg Gly Phe Cys Ala Asn Ser  
125 130 135

Ser Leu Ala Phe Pro Thr Lys Glu Arg Ala Phe Asp Asp Ile Pro  
140 145 150

Asn Ser Glu Leu Ser His Leu Ile Val Asp Asp Arg His Gly Ala  
155 160 165

Ile Tyr Cys Tyr Val Pro Lys Val Ala Cys Thr Asn Trp Lys Arg  
170 175 180

Val Met Ile Val Leu Ser Gly Ser Leu Leu His Arg Gly Ala Pro  
185 190 195

Tyr Arg Asp Pro Leu Arg Ile Pro Arg Glu His Val His Asn Ala  
200 205 210

Ser Ala His Leu Thr Phe Asn Lys Phe Trp Arg Arg Tyr Gly Lys  
215 220 225

Leu Ser Arg His Leu Met Lys Val Lys Leu Lys Lys Tyr Thr Lys  
230 235 240

Phe Leu Phe Val Arg Asp Pro Phe Val Arg Leu Ile Ser Ala Phe  
245 250 255

Arg Ser Lys Phe Glu Leu Glu Asn Glu Glu Phe Tyr Arg Lys Phe  
260 265 270

Ala Val Pro Met Leu Arg Leu Tyr Ala Asn His Thr Ser Leu Pro  
275 280 285

Ala Ser Ala Arg Glu Ala Phe Arg Ala Gly Leu Lys Val Ser Phe  
290 295 300

Ala Asn Phe Ile Gln Tyr Leu Leu Asp Pro His Thr Glu Lys Leu  
305 310 315

Ala Pro Phe Asn Glu His Trp Arg Gln Val Tyr Arg Leu Cys His  
320 325 330

Pro Cys Gln Ile Asp Tyr Asp Phe Val Gly Lys Leu Glu Thr Leu  
335 340 345

Asp Glu Asp Ala Ala Gln Leu Leu Gln Leu Leu Gln Val Asp Arg  
350 355 360

Gln Leu Arg Phe Pro Pro Ser Tyr Arg Asn Arg Thr Ala Ser Ser  
365 370 375

Trp Glu Glu Asp Trp Phe Ala Lys Ile Pro Leu Ala Trp Arg Gln  
380 385 390

Gln Leu Tyr Lys Leu Tyr Glu Ala Asp Phe Val Leu Phe Gly Tyr  
395 400 405

Pro Lys Pro Glu Asn Leu Leu Arg Asp  
410

<210> 467

<211> 1071

<212> DNA

<213> Homo sapiens

<400> 467

tcggggccaga attcggcacg aggcggcacg agggcgacgg cctcacgggg 50

ctttggaggt gaaagaggcc cagagtagag agagagagag accgacgtac 100

acgggatggc tacgggaacg cgctatgccg ggaaggtggt ggtcgtgacc 150

ggggggcgggc gcggcatcgg agctgggatc gtgcgcgcct tcgtgaacag 200

cggggcccga gtggttatct gcgacaagga tgagtctggg ggccggggccc 250

tggagcagga gctccctgga gctgtcttta tcctctgtga tgtgactcag 300

gaagatgatg tgaagaccct ggtttctgag accatccgcc gatttgccg 350

cctggattgt gttgtcaaca acgtggcca ccaccaccc ccacagaggc 400

ctgaggagac ctctgccag ggattccgcc agctgctgga gctgaaccta 450

ctggggacgt acaccttgac caagctcgcc ctcccctacc tgcggaagag 500  
 tcaagggaat gtcatcaaca tctccagcct ggtgggggca atcgccagg 550  
 cccaggcagt tccctatgtg gccaccaagg gggcagtaac agccatgacc 600  
 aaagctttgg ccctggatga aagtccatat ggtgtccgag tcaactgtat 650  
 ctccccagga aacatctgga ccccgctgtg ggaggagctg gcagcctaa 700  
 tgccagaccc tagggccaca atccgagagg gcatgctggc ccagccactg 750  
 ggccgcatgg gccagcccgc tgaggtcggg gctgcggcag tgttctggc 800  
 ctccgaagcc aacttctgca cgggcattga actgctctg acgggggggtg 850  
 cagagctggg gtacgggtgc aaggccagtc ggagcacccc cgtggacgcc 900  
 cccgatatcc ctctctgatt tctctcattt ctactgggg ccccttct 950  
 aggactctcc caccctaaac tccaacctgt atcagatgca gcccctaac 1000  
 ccttagactc taagcccagt tagcaaggtg ccgggtcacc ctgcaggtc 1050  
 ccataaaaac gatttcagc c 1071

<210> 468

<211> 270

<212> PRT

<213> Homo sapiens

<400> 468

Met Ala Thr Gly Thr Arg Tyr Ala Gly Lys Val Val Val Val Thr  
 1 5 10 15

Gly Gly Gly Arg Gly Ile Gly Ala Gly Ile Val Arg Ala Phe Val  
 20 25 30

Asn Ser Gly Ala Arg Val Val Ile Cys Asp Lys Asp Glu Ser Gly  
 35 40 45

Gly Arg Ala Leu Glu Gln Glu Leu Pro Gly Ala Val Phe Ile Leu  
 50 55 60

Cys Asp Val Thr Gln Glu Asp Asp Val Lys Thr Leu Val Ser Glu

65                      70                      75  
Thr Ile Arg Arg Phe Gly Arg Leu Asp Cys Val Val Asn Asn Ala  
80                      85                      90

Gly His His Pro Pro Pro Gln Arg Pro Glu Glu Thr Ser Ala Gln  
95                      100                      105

Gly Phe Arg Gln Leu Leu Glu Leu Asn Leu Leu Gly Thr Tyr Thr  
110                      115                      120

Leu Thr Lys Leu Ala Leu Pro Tyr Leu Arg Lys Ser Gln Gly Asn  
125                      130                      135

Val Ile Asn Ile Ser Ser Leu Val Gly Ala Ile Gly Gln Ala Gln  
140                      145                      150

Ala Val Pro Tyr Val Ala Thr Lys Gly Ala Val Thr Ala Met Thr  
155                      160                      165

Lys Ala Leu Ala Leu Asp Glu Ser Pro Tyr Gly Val Arg Val Asn  
170                      175                      180

Cys Ile Ser Pro Gly Asn Ile Trp Thr Pro Leu Trp Glu Glu Leu  
185                      190                      195

Ala Ala Leu Met Pro Asp Pro Arg Ala Thr Ile Arg Glu Gly Met  
200                      205                      210

Leu Ala Gln Pro Leu Gly Arg Met Gly Gln Pro Ala Glu Val Gly  
215                      220                      225

Ala Ala Ala Val Phe Leu Ala Ser Glu Ala Asn Phe Cys Thr Gly  
230                      235                      240

Ile Glu Leu Leu Val Thr Gly Gly Ala Glu Leu Gly Tyr Gly Cys  
245                      250                      255

Lys Ala Ser Arg Ser Thr Pro Val Asp Ala Pro Asp Ile Pro Ser  
260                      265                      270

<210> 469

<211> 687

<212> DNA

<213> Homo sapiens

<400> 469

aggcgggcag cagctgcagg ctgacctgc agcttggcgg aatggactgg 50  
cctcacaacc tgctgtttct tcttaccatt tccatcttcc tggggctggg 100  
ccagcccagg agccccaaaa gcaagaggaa ggggcaaggg cggcctgggc 150  
ccctggcccc tggccctcac caggtgccac tggacctggt gtcacggatg 200  
aaaccgtatg cccgcatgga ggagtatgag aggaacatcg aggagatggt 250  
ggcccagctg aggaacagct cagagctggc ccagagaaaag tgtgaggtca 300  
acttcagct gtggatgtcc aacaagagga gcctgtctcc ctggggctac 350  
agcatcaacc acgaccccag ccgtatcccc gtggacctgc cggaggcacg 400  
gtgcctgtgt ctgggctgtg tgaaccctt caccatgcag gaggaccgca 450  
gcatggtgag cgtgccggtg ttcagccagg ttctgtgcg ccgccgcctc 500  
tgcccgcac cgccccgcac agggccttgc cgccagcgcg cagtcatgga 550  
gaccatgct gtgggctgca cctgcatctt ctgaatcacc tggcccagaa 600  
gccaggccag cagcccgaga ccacctcct tgcaccttg tgccaagaaa 650  
ggcctatgaa aagtaaacac tgacttttga aagcaag 687

<210> 470

<211> 180

<212> PRT

<213> Homo sapiens

<400> 470

Met Asp Trp Pro His Asn Leu Leu Phe Leu Leu Thr Ile Ser Ile  
1 5 10 15

Phe Leu Gly Leu Gly Gln Pro Arg Ser Pro Lys Ser Lys Arg Lys  
20 25 30

Gly Gln Gly Arg Pro Gly Pro Leu Ala Pro Gly Pro His Gln Val  
35 40 45

Pro Leu Asp Leu Val Ser Arg Met Lys Pro Tyr Ala Arg Met Glu

50	55	60
Glu Tyr Glu Arg Asn Ile Glu Glu Met Val Ala Gln Leu Arg Asn		
65	70	75
Ser Ser Glu Leu Ala Gln Arg Lys Cys Glu Val Asn Leu Gln Leu		
80	85	90
Trp Met Ser Asn Lys Arg Ser Leu Ser Pro Trp Gly Tyr Ser Ile		
95	100	105
Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu Pro Glu Ala Arg		
110	115	120
Cys Leu Cys Leu Gly Cys Val Asn Pro Phe Thr Met Gln Glu Asp		
125	130	135
Arg Ser Met Val Ser Val Pro Val Phe Ser Gln Val Pro Val Arg		
140	145	150
Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr Gly Pro Cys Arg Gln		
155	160	165
Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys Thr Cys Ile Phe		
170	175	180

<210> 471  
 <211> 2368  
 <212> DNA  
 <213> Homo sapiens

<400> 471  
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 aaacccggcg ggcgagcgag gctgcgggcc ggccgctgcc cttccccaca 100  
 ctccccgccg agaagcctcg ctgcgcgcc aacatggcgg gtgggcgctg 150  
 cggcccgag ctaacggcgc tctggccgc ctggatcgcg gctgtggcgg 200  
 cgacggcagg ccccaggag gccgcgctgc cgccggagca gagccgggtc 250  
 cagcccatga ccgcctcaa ctggacgctg gtgatggagg gcgagtggat 300  
 gctgaaattt tacgccccat ggtgtccatc ctgccagcag actgattcag 350



aatgggaggc tttgcaaag aatggtgaaa tacttcagat cagtgtgggg 400  
aaggtagatg tcattcaaga accaggtttg agtggccgct tctttgcac 450  
cactctccca gcatttttc atgcaaagga tgggatattc cgccgttacc 500  
gtggcccagg aatcttcgaa gacctgcaga attatatctt agagaagaaa 550  
tggcaatcag tcgagcctct gactggctgg aaatccccag cttctctaac 600  
gatgtctgga atggctggtc ttttagcat ctctggcaag atatggcatc 650  
ttcacaacta ttcacagtg actcttgaa ttctgcttg gtgttctat 700  
gtgttttcg tcatagccac ctgggtttt ggcctttta tgggtctggt 750  
cttgggtgta atacagaat gttctatgt gccactcca aggcatttat 800  
ctgagcgttc tgagcagaat cggagatcag aggaggctca tagagctgaa 850  
cagttgcagg atgcggagga ggaaaaagat gattcaaatg aagaagaaaa 900  
caaagacagc cttgtagatg atgaagaaga gaaagaagat cttggcgatg 950  
aggatgaagc agaggaagaa gaggaggagg acaacttggc tgctggtgtg 1000  
gatgaggaga gaagtgaggc caatgatcag gggccccag gagaggacgg 1050  
tgtgaccgg gaggaagtag agcctgagga ggctgaagaa ggcattcttg 1100  
agcaaccctg ccagctgac acagaggtgg tggaagactc cttgaggcag 1150  
cgtaaaagtc agcatgctga caagggactg tagatttaat gatgcgtttt 1200  
caagaatata caccaaaaca atatgtcagc ttcccttgg cctgcagttt 1250  
gtaccaaata ctaattttt cctgaatgag caagcttctc ttaaagatg 1300  
ctctctagtc atttggctc atggcagtaa gcctcatgta tactaaggag 1350  
agtcttcag gtgtgacaat caggatatag aaaaacaaac gtagtggttg 1400  
gatctgttg gagactggga tgggaacaag ttcatttact taggggtcag 1450  
agagtctcga ccagaggagg ccattcccag tcctaatacag caccttcag 1500

agacaaggct gcaggccctg tgaaatgaaa gccaagcagg agccttggct 1550  
 cctgagcatc cccaaagtgt aacgtagaag ccttgcattc tttcttgtg 1600  
 taaagtattt attttgcata aattgcagga aacatcaggc accacagtgc 1650  
 atgaaaaatc tttcacagct agaaattgaa agggccttgg gtatagagag 1700  
 cagctcagaa gtcattccag ccctctgaat ctctgtgct atgttttatt 1750  
 tcttaccttt aattttcca gcatttcac catgggcatt caggctctcc 1800  
 acactcttca ctattatctc ttggcagag gactccaata acagccaggt 1850  
 ttacatgaac tgtgttgtt cattctgacc taaggggtt agataatcag 1900  
 taaccataac ccctgaagct gtgactgcca aacatctcaa atgaaatgtt 1950  
 gtggccatca gagactcaaa aggaagtaag gattttacaa gacagattaa 2000  
 aaaaaaattg tttgtccaa aatatagttg ttgtgattt tttttaagt 2050  
 ttctaagca atattttca agccagaagt cctctaagtc ttgccagtac 2100  
 aaggtagtct tgtgaagaaa agttgaatac tgtttgtt tcattcag 2150  
 gggttccctg ggtctgaac tactttaata ataactaaa aaccattct 2200  
 gatttcctt cagtgatgtg ctttgggtga aagaattaat gaactccagt 2250  
 acctgaaagt gaaagattg atttgttc catctctgt aatcttcaa 2300  
 agaattatat cttgtaaat ctctcaatac tcaatctact gtaagtacc 2350  
 agggaggcta atttctt 2368

<210> 472

<211> 349

<212> PRT

<213> Homo sapiens

<400> 472

Met Ala Gly Gly Arg Cys Gly Pro Gln Leu Thr Ala Leu Leu Ala

1

5

10

15

Ala Trp Ile Ala Ala Val Ala Ala Thr Ala Gly Pro Glu Glu Ala  
20 25 30

Ala Leu Pro Pro Glu Gln Ser Arg Val Gln Pro Met Thr Ala Ser  
35 40 45

Asn Trp Thr Leu Val Met Glu Gly Glu Trp Met Leu Lys Phe Tyr  
50 55 60

Ala Pro Trp Cys Pro Ser Cys Gln Gln Thr Asp Ser Glu Trp Glu  
65 70 75

Ala Phe Ala Lys Asn Gly Glu Ile Leu Gln Ile Ser Val Gly Lys  
80 85 90

Val Asp Val Ile Gln Glu Pro Gly Leu Ser Gly Arg Phe Phe Val  
95 100 105

Thr Thr Leu Pro Ala Phe Phe His Ala Lys Asp Gly Ile Phe Arg  
110 115 120

Arg Tyr Arg Gly Pro Gly Ile Phe Glu Asp Leu Gln Asn Tyr Ile  
125 130 135

Leu Glu Lys Lys Trp Gln Ser Val Glu Pro Leu Thr Gly Trp Lys  
140 145 150

Ser Pro Ala Ser Leu Thr Met Ser Gly Met Ala Gly Leu Phe Ser  
155 160 165

Ile Ser Gly Lys Ile Trp His Leu His Asn Tyr Phe Thr Val Thr  
170 175 180

Leu Gly Ile Pro Ala Trp Cys Ser Tyr Val Phe Phe Val Ile Ala  
185 190 195

Thr Leu Val Phe Gly Leu Phe Met Gly Leu Val Leu Val Val Ile  
200 205 210

Ser Glu Cys Phe Tyr Val Pro Leu Pro Arg His Leu Ser Glu Arg  
215 220 225

Ser Glu Gln Asn Arg Arg Ser Glu Glu Ala His Arg Ala Glu Gln  
230 235 240

Leu Gln Asp Ala Glu Glu Glu Lys Asp Asp Ser Asn Glu Glu Glu  
245 250 255

Asn Lys Asp Ser Leu Val Asp Asp Glu Glu Glu Lys Glu Asp Leu  
260 265 270

Gly Asp Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu Asp Asn Leu  
275 280 285

Ala Ala Gly Val Asp Glu Glu Arg Ser Glu Ala Asn Asp Gln Gly  
290 295 300

Pro Pro Gly Glu Asp Gly Val Thr Arg Glu Glu Val Glu Pro Glu  
305 310 315

Glu Ala Glu Glu Gly Ile Ser Glu Gln Pro Cys Pro Ala Asp Thr  
320 325 330

Glu Val Val Glu Asp Ser Leu Arg Gln Arg Lys Ser Gln His Ala  
335 340 345

Asp Lys Gly Leu

<210> 473

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 473

gtccagccca tgaccgcctc caac 24

<210> 474

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 474

ctctctcat ccacaccagc agcc 24

<210> 475

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 475

gtggatgctg aaattttacg ccccatgggtg tccatcctgc cagc 44

<210> 476

<211> 2478

<212> DNA

<213> Homo sapiens

<400> 476

atctggttga actacttaag cttaatttgt taaactccgg taagtaccta 50

gcccacatga ttgactcag agattctctt ttgtccacag acagtcatt 100

caggggcaga aagaaaagag ctcccaaatg ctatatctat tcaggggctc 150

tcaagaacaa tggaatatca tcctgattta gaaaatttgg atgaagatgg 200

atatactcaa ttacacttcg actctcaaag caataccagg atagctgttg 250

tttcagagaa aggatcgtgt gctgcatctc ctcttggcg cctcattgct 300

gtaattttgg gaatcctatg ctggtaata ctggtgatag ctgtggctct 350

gggtaccatg ggggttcttt ccagcccttg tcctcctaatt tggattatat 400

atgagaagag ctgttatcta ttcagcatgt cactaaattc ctgggatgga 450

agtaaaagac aatgctggca actgggctct aatctcctaa agatagacag 500

ctcaaatgaa ttgggattta tagtaaaaca agtgtcttcc caacctgata 550

attcattttg gataggcctt tctcgcccc agactgaggt accatggctc 600

tgggaggatg gatcaacatt ctcttctaac ttatttcaga tcagaaccac 650

agctacccaa gaaaacccat ctccaaattg tgtatggatt cacgtgtcag 700

tcatttatga ccaactgtgt agtgtgccct catatagtat ttgtgagaag 750

aagttttcaa tgtaagagga aggggtggaga aggagagaga aatatgtgag 800

gtagtaagga ggacagaaaa cagaacagaa aagagtaaca gctgaggtca 850

agataaatgc agaaaatgtt tagagagcct ggccaactgt aatcttaacc 900

aagaaattga agggagaggc tgtgatttct gtattgtcg acctacaggt 950

aggctagtat tatttttcta gttagtagat ccctagacat ggaatcaggg 1000

cagccaagct tgagttttta tttttattt atttatttt ttgagatagg 1050

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tgcagtatc tctcgctca gcccctcaag tagctgggac tacaggtgca 1150

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gccatgttga ccaagctggt ctctaactcc tgggcttaag tgatctgccc 1250

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cttctagcag tatatcagtt atgaactgag ggtgaaatat atttctgaat 1500

agctaaatga agaaatggga aaaaatcttc accacagtca gagcaatttt 1550

attattttca tcagtatgat cataattatg attatcatct tagtaaaaag 1600

caggaactcc tactttttct ttatcaatta aatagctcag agagtacatc 1650

tgccatatct ctaatagaat ctttttttt ttttttttt ttgagacag 1700

agtttcgctc ttgttgccca ggctggagtg caacggcacg atctcggctc 1750

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caagtagctg ggattacagt caggcaccac cacacccggc taattttgta 1850

ttttttagt agagacaggg ttctccatg tcggtcaggg tagtcccga 1900  
 ctctgacct caagtgatct gcctgcctcg gcctcccaag tgctgggatt 1950  
 acaggcgtga gccactgcac ccagcctaga atctgtata atatgtaatt 2000  
 gtagggaaac tgctctcata ggaaagtttt ctgcttttta aatacaaaaa 2050  
 tacataaaaa tacataaaat ctgatgatga atataaaaaa gtaaccaacc 2100  
 tcattggaac aagtattaac atttggaat atgttttatt agttttgtga 2150  
 tgtactgttt tacaattttt accatttttt tcagtaatta ctgtaaaatg 2200  
 gtattattgg aatgaaacta tatttcctca tgtctgatt tgccttattt 2250  
 ttttcatact ttccactgg tgctattttt attccaatg gatatttctg 2300  
 tattactagg gaggcattta cagtcctcta atgttgatta atatgtgaaa 2350  
 agaaattgta ccaattttac taaattatgc agtttaaaat ggatgatttt 2400  
 atgttatgtg gatttcattt caataaaaaa aaactcttat caaaaaaaaaa 2450  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2478

<210> 477  
 <211> 201  
 <212> PRT  
 <213> Homo sapiens

<400> 477  
 Met Glu Tyr His Pro Asp Leu Glu Asn Leu Asp Glu Asp Gly Tyr  
 1 5 10 15  
 Thr Gln Leu His Phe Asp Ser Gln Ser Asn Thr Arg Ile Ala Val  
 20 25 30  
 Val Ser Glu Lys Gly Ser Cys Ala Ala Ser Pro Pro Trp Arg Leu  
 35 40 45  
 Ile Ala Val Ile Leu Gly Ile Leu Cys Leu Val Ile Leu Val Ile  
 50 55 60  
 Ala Val Val Leu Gly Thr Met Gly Val Leu Ser Ser Pro Cys Pro

65	70	75
Pro Asn Trp Ile Ile Tyr Glu Lys Ser Cys Tyr Leu Phe Ser Met		
80	85	90
Ser Leu Asn Ser Trp Asp Gly Ser Lys Arg Gln Cys Trp Gln Leu		
95	100	105
Gly Ser Asn Leu Leu Lys Ile Asp Ser Ser Asn Glu Leu Gly Phe		
110	115	120
Ile Val Lys Gln Val Ser Ser Gln Pro Asp Asn Ser Phe Trp Ile		
125	130	135
Gly Leu Ser Arg Pro Gln Thr Glu Val Pro Trp Leu Trp Glu Asp		
140	145	150
Gly Ser Thr Phe Ser Ser Asn Leu Phe Gln Ile Arg Thr Thr Ala		
155	160	165
Thr Gln Glu Asn Pro Ser Pro Asn Cys Val Trp Ile His Val Ser		
170	175	180
Val Ile Tyr Asp Gln Leu Cys Ser Val Pro Ser Tyr Ser Ile Cys		
185	190	195
Glu Lys Lys Phe Ser Met		
200		

<210> 478

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 478

gtccacagac agtcattca ggagcag 27

<210> 479

<211> 20

<212> DNA

<213> Artificial Sequence



<220>

<223> Synthetic oligonucleotide probe

<400> 479

acaagtgtct tcccaacctg 20

<210> 480

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 480

atcctcccag agccatggta cctc 24

<210> 481

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 481

ccaaggatag ctgtgtttc agagaaagga tcgtgtgctg catctcctcc 50

t 51

<210> 482

<211> 3819

<212> DNA

<213> Homo sapiens

<400> 482

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agacctggag ggtctcgctc tgtcacacag gctggagtgc agtgggtga 100

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<211> 693

<212> PRT

<213> Homo sapiens

<400> 483

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Asp Phe Arg Phe Cys Ser Gln Arg Asn Gln Thr His Arg Ser Ser  
35 40 45

Leu His Tyr Lys Pro Thr Pro Asp Leu Arg Ile Ser Ile Glu Asn  
50 55 60

Ser Glu Glu Ala Leu Thr Val His Ala Pro Phe Pro Ala Ala His  
65 70 75

Pro Ala Ser Arg Ser Phe Pro Asp Pro Arg Gly Leu Tyr His Phe  
80 85 90

Cys Leu Tyr Trp Asn Arg His Ala Gly Arg Leu His Leu Leu Tyr  
95 100 105

Gly Lys Arg Asp Phe Leu Leu Ser Asp Lys Ala Ser Ser Leu Leu  
110 115 120

Cys Phe Gln His Gln Glu Glu Ser Leu Ala Gln Gly Pro Pro Leu  
125 130 135

Leu Ala Thr Ser Val Thr Ser Trp Trp Ser Pro Gln Asn Ile Ser  
140 145 150

Leu Pro Ser Ala Ala Ser Phe Thr Phe Ser Phe His Ser Pro Pro  
155 160 165

His Thr Ala Ala His Asn Ala Ser Val Asp Met Cys Glu Leu Lys  
170 175 180

Arg Asp Leu Gln Leu Leu Ser Gln Phe Leu Lys His Pro Gln Lys  
185 190 195

Ala Ser Arg Arg Pro Ser Ala Ala Pro Ala Ser Gln Gln Leu Gln  
200 205 210

Ser Leu Glu Ser Lys Leu Thr Ser Val Arg Phe Met Gly Asp Met  
215 220 225

Val Ser Phe Glu Glu Asp Arg Ile Asn Ala Thr Val Trp Lys Leu  
230 235 240

Gln Pro Thr Ala Gly Leu Gln Asp Leu His Ile His Ser Arg Gln  
245 250 255

Glu Glu Glu Gln Ser Glu Ile Met Glu Tyr Ser Val Leu Leu Pro  
260 265 270

Arg Thr Leu Phe Gln Arg Thr Lys Gly Arg Ser Gly Glu Ala Glu  
275 280 285

Lys Arg Leu Leu Leu Val Asp Phe Ser Ser Gln Ala Leu Phe Gln  
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Asp Lys Asn Ser Ser Gln Val Leu Gly Glu Lys Val Leu Gly Ile  
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Val Val Gln Asn Thr Lys Val Ala Asn Leu Thr Glu Pro Val Val  
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Cys Val Phe Trp Val Glu Asp Pro Thr Leu Ser Ser Pro Gly His  
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Trp Ser Ser Ala Gly Cys Glu Thr Val Arg Arg Glu Thr Gln Thr  
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Ser Cys Phe Cys Asn His Leu Thr Tyr Phe Ala Val Leu Met Val  
380 385 390

Ser Ser Val Glu Val Asp Ala Val His Lys His Tyr Leu Ser Leu  
395 400 405

Leu Ser Tyr Val Gly Cys Val Val Ser Ala Leu Ala Cys Leu Val  
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Thr Ile Ala Ala Tyr Leu Cys Ser Arg Val Pro Leu Pro Cys Arg  
425 430 435

Arg Lys Pro Arg Asp Tyr Thr Ile Lys Val His Met Asn Leu Leu  
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Val Ala Leu Thr Gly Ser Glu Ala Gly Cys Arg Ala Ser Ala Ile  
470 475 480

Phe Leu His Phe Ser Leu Leu Thr Cys Leu Ser Trp Met Gly Leu  
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Glu Gly Tyr Asn Leu Tyr Arg Leu Val Val Glu Val Phe Gly Thr  
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Tyr Val Pro Gly Tyr Leu Leu Lys Leu Ser Ala Met Gly Trp Gly  
515 520 525

Phe Pro Ile Phe Leu Val Thr Leu Val Ala Leu Val Asp Val Asp  
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Asn Tyr Gly Pro Ile Ile Leu Ala Val His Arg Thr Pro Glu Gly  
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Val Ile Tyr Pro Ser Met Cys Trp Ile Arg Asp Ser Leu Val Ser  
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Tyr Ile Thr Asn Leu Gly Leu Phe Ser Leu Val Phe Leu Phe Asn  
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Met Ala Met Leu Ala Thr Met Val Val Gln Ile Leu Arg Leu Arg  
590 595 600

Pro His Thr Gln Lys Trp Ser His Val Leu Thr Leu Leu Gly Leu  
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Ser Leu Val Leu Gly Leu Pro Trp Ala Leu Ile Phe Phe Ser Phe  
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Ala Ser Gly Thr Phe Gln Leu Val Val Leu Tyr Leu Phe Ser Ile  
635 640 645

Ile Thr Ser Phe Gln Gly Phe Leu Ile Phe Ile Trp Tyr Trp Ser  
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Ser Asp Ser Ala Arg Leu Pro Ile Ser Ser Gly Ser Thr Ser Ser  
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Ser Arg Ile

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<211> 516

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<213> Homo sapiens

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<223> unknown base

<400> 484

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<223> Synthetic oligonucleotide probe

<400> 485

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<210> 486

<211> 24

<212> DNA

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<400> 486

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<212> DNA

<213> Homo sapiens

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<221> unsure

<222> 2715

<223> unknown base

<400> 487

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 Pro Arg Phe Pro His Thr Tyr Pro Arg Asn Thr Val Leu Val Trp  
 65 70 75  
 Arg Leu Val Ala Val Glu Glu Asn Val Trp Ile Gln Leu Thr Phe  
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 Asp Glu Arg Phe Gly Leu Glu Asp Pro Glu Asp Asp Ile Cys Lys  
 95 100 105  
 Tyr Asp Phe Val Glu Val Glu Glu Pro Ser Asp Gly Thr Ile Leu  
 110 115 120

Gly Arg Trp Cys Gly Ser Gly Thr Val Pro Gly Lys Gln Ile Ser  
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Lys Gly Asn Gln Ile Arg Ile Arg Phe Val Ser Asp Glu Tyr Phe  
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Pro Ser Glu Pro Gly Phe Cys Ile His Tyr Asn Ile Val Met Pro  
155 160 165

Gln Phe Thr Glu Ala Val Ser Pro Ser Val Leu Pro Pro Ser Ala  
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Leu Pro Leu Asp Leu Leu Asn Asn Ala Ile Thr Ala Phe Ser Thr  
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Leu Glu Asp Leu Ile Arg Tyr Leu Glu Pro Glu Arg Trp Gln Leu  
200 205 210

Asp Leu Glu Asp Leu Tyr Arg Pro Thr Trp Gln Leu Leu Gly Lys  
215 220 225

Ala Phe Val Phe Gly Arg Lys Ser Arg Val Val Asp Leu Asn Leu  
230 235 240

Leu Thr Glu Glu Val Arg Leu Tyr Ser Cys Thr Pro Arg Asn Phe  
245 250 255

Ser Val Ser Ile Arg Glu Glu Leu Lys Arg Thr Asp Thr Ile Phe  
260 265 270

Trp Pro Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn Cys Ala  
275 280 285

Cys Cys Leu His Asn Cys Asn Glu Cys Gln Cys Val Pro Ser Lys  
290 295 300

Val Thr Lys Lys Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr  
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<223> Synthetic oligonucleotide probe

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<212> DNA

<213> Artificial Sequence

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<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 491

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<223> Synthetic oligonucleotide probe

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<210> 493

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 His Val Ile Val Asp Cys Thr Asp Lys His Leu Thr Glu Ile Pro  
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 Gly Gly Ile Pro Thr Asn Thr Thr Asn Leu Thr Leu Thr Ile Asn  
 65 70 75  
 His Ile Pro Asp Ile Ser Pro Ala Ser Phe His Arg Leu Asp His  
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Leu Val Glu Ile Asp Phe Arg Cys Asn Cys Val Pro Ile Pro Leu  
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Gly Ser Lys Asn Asn Met Cys Ile Lys Arg Leu Gln Ile Lys Pro  
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Arg Ser Phe Ser Gly Leu Thr Tyr Leu Lys Ser Leu Tyr Leu Asp  
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Gly Asn Gln Leu Leu Glu Ile Pro Gln Gly Leu Pro Pro Ser Leu  
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Gln Leu Leu Ser Leu Glu Ala Asn Asn Ile Phe Ser Ile Arg Lys  
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Glu Asn Leu Thr Glu Leu Ala Asn Ile Glu Ile Leu Tyr Leu Gly  
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Gln Asn Cys Tyr Tyr Arg Asn Pro Cys Tyr Val Ser Tyr Ser Ile  
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Glu Lys Asp Ala Phe Leu Asn Leu Thr Lys Leu Lys Val Leu Ser  
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Leu Lys Asp Asn Asn Val Thr Ala Val Pro Thr Val Leu Pro Ser  
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Thr Leu Thr Glu Leu Tyr Leu Tyr Asn Asn Met Ile Ala Lys Ile  
230 235 240

Gln Glu Asp Asp Phe Asn Asn Leu Asn Gln Leu Gln Ile Leu Asp  
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Leu Ser Gly Asn Cys Pro Arg Cys Tyr Asn Ala Pro Phe Pro Cys  
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Ala Pro Cys Lys Asn Asn Ser Pro Leu Gln Ile Pro Val Asn Ala  
275 280 285

Phe Asp Ala Leu Thr Glu Leu Lys Val Leu Arg Leu His Ser Asn  
290 295 300

Ser Leu Gln His Val Pro Pro Arg Trp Phe Lys Asn Ile Asn Lys  
305 310 315

Leu Gln Glu Leu Asp Leu Ser Gln Asn Phe Leu Ala Lys Glu Ile  
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Gly Asp Ala Lys Phe Leu His Phe Leu Pro Ser Leu Ile Gln Leu  
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Asn Leu Ser Gln Ala Phe Ser Ser Leu Lys Ser Leu Lys Ile Leu  
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Arg Ile Arg Gly Tyr Val Phe Lys Glu Leu Lys Ser Phe Asn Leu  
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Ser Pro Leu His Asn Leu Gln Asn Leu Glu Val Leu Asp Leu Gly  
395 400 405

Thr Asn Phe Ile Lys Ile Ala Asn Leu Ser Met Phe Lys Gln Phe  
410 415 420

Lys Arg Leu Lys Val Ile Asp Leu Ser Val Asn Lys Ile Ser Pro  
425 430 435

Ser Gly Asp Ser Ser Glu Val Gly Phe Cys Ser Asn Ala Arg Thr  
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Ser Val Glu Ser Tyr Glu Pro Gln Val Leu Glu Gln Leu His Tyr  
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Phe Arg Tyr Asp Lys Tyr Ala Arg Ser Cys Arg Phe Lys Asn Lys  
470 475 480

Glu Ala Ser Phe Met Ser Val Asn Glu Ser Cys Tyr Lys Tyr Gly  
485 490 495

Gln Thr Leu Asp Leu Ser Lys Asn Ser Ile Phe Phe Val Lys Ser  
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Ser Asp Phe Gln His Leu Ser Phe Leu Lys Cys Leu Asn Leu Ser  
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Gly Asn Leu Ile Ser Gln Thr Leu Asn Gly Ser Glu Phe Gln Pro  
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Thr His Met Leu Asn Phe Thr Lys Asn Leu Lys Val Leu Gln Lys  
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Phe Lys Asn Leu Leu Lys Leu Glu Glu Leu Asp Ile Ser Lys Asn  
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680 685 690

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695 700 705

Leu Ser His Asn Gln Leu Thr Thr Val Pro Glu Arg Leu Ser Asn  
710 715 720

Cys Ser Arg Ser Leu Lys Asn Leu Ile Leu Lys Asn Asn Gln Ile  
725 730 735

Arg Ser Leu Thr Lys Tyr Phe Leu Gln Asp Ala Phe Gln Leu Arg  
740 745 750

Tyr Leu Asp Leu Ser Ser Asn Lys Ile Gln Met Ile Gln Lys Thr  
755 760 765

Ser Phe Pro Glu Asn Val Leu Asn Asn Leu Lys Met Leu Leu Leu  
770 775 780

His His Asn Arg Phe Leu Cys Thr Cys Asp Ala Val Trp Phe Val  
785 790 795

Trp Trp Val Asn His Thr Glu Val Thr Ile Pro Tyr Leu Ala Thr  
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830 835 840

Ile Leu Phe Ser Leu Ser Ile Ser Val Ser Leu Phe Leu Met Val  
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860 865 870

Tyr His Phe Cys Lys Ala Lys Ile Lys Gly Tyr Gln Arg Leu Ile  
875 880 885

Ser Pro Asp Cys Cys Tyr Asp Ala Phe Ile Val Tyr Asp Thr Lys  
890 895 900

Asp Pro Ala Val Thr Glu Trp Val Leu Ala Glu Leu Val Ala Lys  
905 910 915

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920 925 930

Arg Asp Trp Leu Pro Gly Gln Pro Val Leu Glu Asn Leu Ser Gln  
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950 955 960

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965 970 975

Gln Arg Leu Met Asp Glu Lys Val Asp Val Ile Ile Leu Ile Phe  
980 985 990

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Arg Leu Cys Gly Ser Ser Val Leu Glu Trp Pro Thr Asn Pro Gln  
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<211> 4199

<212> DNA

<213> Homo sapiens

<400> 497

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<211> 1041

<212> PRT

<213> Homo sapiens

<400> 498

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35 40 45

Ile Ala Glu Cys Ser Asn Arg Arg Leu Gln Glu Val Pro Gln Thr

50 55 60

Val Gly Lys Tyr Val Thr Glu Leu Asp Leu Ser Asp Asn Phe Ile

65 70 75

Thr His Ile Thr Asn Glu Ser Phe Gln Gly Leu Gln Asn Leu Thr

80 85 90

Lys Ile Asn Leu Asn His Asn Pro Asn Val Gln His Gln Asn Gly

95 100 105

Asn Pro Gly Ile Gln Ser Asn Gly Leu Asn Ile Thr Asp Gly Ala

110 115 120

Phe Leu Asn Leu Lys Asn Leu Arg Glu Leu Leu Leu Glu Asp Asn

125 130 135

Gln Leu Pro Gln Ile Pro Ser Gly Leu Pro Glu Ser Leu Thr Glu

140 145 150

Leu Ser Leu Ile Gln Asn Asn Ile Tyr Asn Ile Thr Lys Glu Gly

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Ile Ser Arg Leu Ile Asn Leu Lys Asn Leu Tyr Leu Ala Trp Asn

170 175 180

Cys Tyr Phe Asn Lys Val Cys Glu Lys Thr Asn Ile Glu Asp Gly

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215	220	225
Lys Leu Phe Leu Ser Asn Thr Gln Ile Lys Tyr Ile Ser Glu Glu		
230	235	240
Asp Phe Lys Gly Leu Ile Asn Leu Thr Leu Leu Asp Leu Ser Gly		
245	250	255
Asn Cys Pro Arg Cys Phe Asn Ala Pro Phe Pro Cys Val Pro Cys		
260	265	270
Asp Gly Gly Ala Ser Ile Asn Ile Asp Arg Phe Ala Phe Gln Asn		
275	280	285
Leu Thr Gln Leu Arg Tyr Leu Asn Leu Ser Ser Thr Ser Leu Arg		
290	295	300
Lys Ile Asn Ala Ala Trp Phe Lys Asn Met Pro His Leu Lys Val		
305	310	315
Leu Asp Leu Glu Phe Asn Tyr Leu Val Gly Glu Ile Val Ser Gly		
320	325	330
Ala Phe Leu Thr Met Leu Pro Arg Leu Glu Ile Leu Asp Leu Ser		
335	340	345
Phe Asn Tyr Ile Lys Gly Ser Tyr Pro Gln His Ile Asn Ile Ser		
350	355	360
Arg Asn Phe Ser Lys Leu Leu Ser Leu Arg Ala Leu His Leu Arg		
365	370	375
Gly Tyr Val Phe Gln Glu Leu Arg Glu Asp Asp Phe Gln Pro Leu		
380	385	390
Met Gln Leu Pro Asn Leu Ser Thr Ile Asn Leu Gly Ile Asn Phe		
395	400	405
Ile Lys Gln Ile Asp Phe Lys Leu Phe Gln Asn Phe Ser Asn Leu		

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Asp Thr Arg Gln Ser Tyr Ala Asn Ser Ser Ser Phe Gln Arg His		
440	445	450
Ile Arg Lys Arg Arg Ser Thr Asp Phe Glu Phe Asp Pro His Ser		
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Asn Phe Tyr His Phe Thr Arg Pro Leu Ile Lys Pro Gln Cys Ala		
470	475	480
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Ile Gly Pro Asn Gln Phe Glu Asn Leu Pro Asp Ile Ala Cys Leu		
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Phe Ser Ala Ile Pro His Val Lys Tyr Leu Asp Leu Thr Asn Asn		
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Arg Leu Asp Phe Asp Asn Ala Ser Ala Leu Thr Glu Leu Ser Asp		
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Leu Glu Val Leu Asp Leu Ser Tyr Asn Ser His Tyr Phe Arg Ile		
560	565	570
Ala Gly Val Thr His His Leu Glu Phe Ile Gln Asn Phe Thr Asn		
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Leu Lys Val Leu Asn Leu Ser His Asn Asn Ile Tyr Thr Leu Thr		
590	595	600
Asp Lys Tyr Asn Leu Glu Ser Lys Ser Leu Val Glu Leu Val Phe		
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Ser Gly Asn Arg Leu Asp Ile Leu Trp Asn Asp Asp Asp Asn Arg		
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Tyr Ile Ser Ile Phe Lys Gly Leu Lys Asn Leu Thr Arg Leu Asp		

635	640	645
Leu Ser Leu Asn Arg Leu Lys His Ile Pro Asn Glu Ala Phe Leu		
650	655	660
Asn Leu Pro Ala Ser Leu Thr Glu Leu His Ile Asn Asp Asn Met		
665	670	675
Leu Lys Phe Phe Asn Trp Thr Leu Leu Gln Gln Phe Pro Arg Leu		
680	685	690
Glu Leu Leu Asp Leu Arg Gly Asn Lys Leu Leu Phe Leu Thr Asp		
695	700	705
Ser Leu Ser Asp Phe Thr Ser Ser Leu Arg Thr Leu Leu Leu Ser		
710	715	720
His Asn Arg Ile Ser His Leu Pro Ser Gly Phe Leu Ser Glu Val		
725	730	735
Ser Ser Leu Lys His Leu Asp Leu Ser Ser Asn Leu Leu Lys Thr		
740	745	750
Ile Asn Lys Ser Ala Leu Glu Thr Lys Thr Thr Lys Leu Ser		
755	760	765
Met Leu Glu Leu His Gly Asn Pro Phe Glu Cys Thr Cys Asp Ile		
770	775	780
Gly Asp Phe Arg Arg Trp Met Asp Glu His Leu Asn Val Lys Ile		
785	790	795
Pro Arg Leu Val Asp Val Ile Cys Ala Ser Pro Gly Asp Gln Arg		
800	805	810
Gly Lys Ser Ile Val Ser Leu Glu Leu Thr Thr Cys Val Ser Asp		
815	820	825
Val Thr Ala Val Ile Leu Phe Phe Phe Thr Phe Phe Ile Thr Thr		
830	835	840
Met Val Met Leu Ala Ala Leu Ala His His Leu Phe Tyr Trp Asp		
845	850	855
Val Trp Phe Ile Tyr Asn Val Cys Leu Ala Lys Val Lys Gly Tyr		

860	865	870
Arg Ser Leu Ser Thr Ser Gln Thr Phe Tyr Asp Ala Tyr Ile Ser		
875	880	885
Tyr Asp Thr Lys Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu		
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Leu Arg Tyr His Leu Glu Glu Ser Arg Asp Lys Asn Val Leu Leu		
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Cys Leu Glu Glu Arg Asp Trp Asp Pro Gly Leu Ala Ile Ile Asp		
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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 502

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 503

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<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 503



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<223> Synthetic oligonucleotide probe

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<210> 505

<211> 1738

<212> DNA

<213> Homo sapiens

<400> 505

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gtgcctccag gcggccagtg ggctgaggc cccagcaagg gctagggtcc 200

atctccagtc ccaggacaca gcagcggcca ccatggccac gcctgggctc 250

cagcagcatc agcagcccc aggaccgggg aggcacaggt ggccccacc 300

accggagga gcagctctg cccctgtccg ggggatgact gattctctc 350

cgccaggcca cccagaggag aaggccacc cgctggagg cacaggccat 400

gaggggtct caggaggtgc tgctgatgtg gcttctggtg ttggcagtgg 450

gcggcacaga gcacgcctac cgccccggcc gtagggtgtg tgctgtccgg 500

gctcacgggg accctgtctc cgagtcgttc gtgcagcgtg tgtaccagcc 550

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<211> 273

<212> PRT

<213> Homo sapiens

<400> 506

Met Arg Gly Ser Gln Glu Val Leu Leu Met Trp Leu Leu Val Leu  
1 5 10 15

Ala Val Gly Gly Thr Glu His Ala Tyr Arg Pro Gly Arg Arg Val  
20 25 30

Cys Ala Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val  
35 40 45

Gln Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg  
50 55 60

Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg  
65 70 75

Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro  
80 85 90

Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala  
95 100 105

Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro  
110 115 120

Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln  
125 130 135

Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Gln  
140 145 150

Arg Cys Ile Asn Thr Ala Gly Ser Tyr Trp Cys Gln Cys Trp Glu  
155 160 165

Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys Val Pro Lys Gly  
170 175 180

Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala  
185 190 195

Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu

200	205	210
Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu Ala		
215	220	225
Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu		
230	235	240
Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu		
245	250	255
Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys		
260	265	270

Lys Asp Ser

<210> 507

<211> 1700

<212> DNA

<213> Homo sapiens

<400> 507

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ccaccatggc cacgcctggg ctccagcagc atcagagcag ccctgtggt 150

tggcagcaaa gttagcttg gctgggcccg ctgtgagggg cttagcgcta 200

cgcctgcgg tgtcccgagg gctgaggtct cctcatcttc tccctagcag 250

tggatgagca acccaacggg ggcccgggga ggggaactgg ccccgaggga 300

gaggaacccc aaagccacat ctgtagccag gatgagcagt gtgaatccag 350

gcagccccca ggaccgggga ggcacaggtg gccccacca cccggaggag 400

cagctcctgc ccctgtccgg gggatgactg attctcctcc gccaggccac 450

ccagaggaga aggccacccc gcctggaggc acaggccatg aggggctctc 500

aggaggtgct gctgatgtgg ctctggtgt tggcagtggg cggcacagag 550

cacgcctacc ggccccggccg tagggtgtgt gctgtccggg ctcacgggga 600  
ccctgtctcc gagtgttcg tgcagcgtgt gtaccagccc ttcctacca 650  
cctgcgacgg gcaccgggcc tgcagcacct accgaacat ctataggacc 700  
gcctaccgcc gcagccctgg gctggcccct gccaggcctc gctacgcgtg 750  
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caatatgcca gccgcatgc cggaacggag ggagctgtgt ccagcctggc 850  
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tccaaggcc aggtggaccc tcagctgagg gaaggtacga gctccctgct 1600  
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cctcagtggg ggctgctgcc tgacccccag cacaataaaa atgaaacgtg 1700

<210> 508

<211> 1538

<212> DNA

<213> Homo sapiens

<400> 508

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ctgaggcccc agcaagggtt agggctccatc tccagtccca ggacacagca 150  
ggggccacca tggccacgcc tgggtccag cagcatcagc agccccagg 200  
accggggagg cacaggtggc cccaccacc cggaggagca gctcctgcc 250  
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gccacccgc ctggaggcac aggcatgag gggctctcag gagtgctgc 350  
tgatgtggct tctggtgtg gcagtgggc gcacagagca cgcctaccg 400  
cccgccgta ggggtgtgc tgcggggct cacggggacc ctgtctccga 450  
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accgggcctg cagcacctac cgaacctct ataggaccgc ctaccgccg 550  
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tgtgtgcca agggaggggc cccagggtg gcccacaacc cgacaggagt 900  
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<210> 509

<211> 273

<212> PRT

<213> Homo sapiens

<400> 509

Met Arg Gly Ser Gln Glu Val Leu Leu Met Trp Leu Leu Val Leu

1 5 10 15

Ala Val Gly Gly Thr Glu His Ala Tyr Arg Pro Gly Arg Arg Val

20 25 30

Cys Ala Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val

35 40 45

Gln Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg

50 55 60

Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg

65 70 75

Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro  
80 85 90

Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala  
95 100 105

Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro  
110 115 120

Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln  
125 130 135

Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Gln  
140 145 150

Arg Cys Val Asn Thr Ala Gly Ser Tyr Trp Cys Gln Cys Trp Glu  
155 160 165

Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys Val Pro Lys Gly  
170 175 180

Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala  
185 190 195

Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu  
200 205 210

Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu Ala  
215 220 225

Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu  
230 235 240

Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu  
245 250 255

Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys  
260 265 270

Lys Asp Ser

<210> 510

<211> 21

<212> DNA



<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 510

tggagcagca atatgccagc c 21

<210> 511

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 511

tttccactc ctgtcgggtt gg 22

<210> 512

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 512

ggtgacactt gccagtcaga tgtggatgaa tgcagtgcta ggaggg 46

<210> 513

<211> 2690

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 2039-2065

<223> unknown base

<400> 513

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cccgtgggc cggtttatcg ggaggagatt gtctccagg gctagcaatt 250  
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<210> 514

<211> 364

<212> PRT

<213> Homo sapiens

<400> 514

Met Ser Val Met Val Val Arg Lys Lys Val Thr Arg Lys Trp Glu  
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Lys Leu Pro Gly Arg Asn Thr Phe Cys Cys Asp Gly Arg Val Met  
 20 25 30

Met Ala Arg Gln Lys Gly Ile Phe Tyr Leu Thr Leu Phe Leu Ile  
 35 40 45

Leu Gly Thr Cys Thr Leu Phe Phe Ala Phe Glu Cys Arg Tyr Leu  
 50 55 60

Ala Val Gln Leu Ser Pro Ala Ile Pro Val Phe Ala Ala Met Leu  
 65 70 75

Phe Leu Phe Ser Met Ala Thr Leu Leu Arg Thr Ser Phe Ser Asp  
 80 85 90

Pro Gly Val Ile Pro Arg Ala Leu Pro Asp Glu Ala Ala Phe Ile  
 95 100 105

Glu Met Glu Ile Glu Ala Thr Asn Gly Ala Val Pro Gln Gly Gln  
 110 115 120

Arg Pro Pro Pro Arg Ile Lys Asn Phe Gln Ile Asn Asn Gln Ile  
 125 130 135

Val Lys Leu Lys Tyr Cys Tyr Thr Cys Lys Ile Phe Arg Pro Pro  
140 145 150

Arg Ala Ser His Cys Ser Ile Cys Asp Asn Cys Val Glu Arg Phe  
155 160 165

Asp His His Cys Pro Trp Val Gly Asn Cys Val Gly Lys Arg Asn  
170 175 180

Tyr Arg Tyr Phe Tyr Leu Phe Ile Leu Ser Leu Ser Leu Leu Thr  
185 190 195

Ile Tyr Val Phe Ala Phe Asn Ile Val Tyr Val Ala Leu Lys Ser  
200 205 210

Leu Lys Ile Gly Phe Leu Glu Thr Leu Lys Glu Thr Pro Gly Thr  
215 220 225

Val Leu Glu Val Leu Ile Cys Phe Phe Thr Leu Trp Ser Val Val  
230 235 240

Gly Leu Thr Gly Phe His Thr Phe Leu Val Ala Leu Asn Gln Thr  
245 250 255

Thr Asn Glu Asp Ile Lys Gly Ser Trp Thr Gly Lys Asn Arg Val  
260 265 270

Gln Asn Pro Tyr Ser His Gly Asn Ile Val Lys Asn Cys Cys Glu  
275 280 285

Val Leu Cys Gly Pro Leu Pro Pro Ser Val Leu Asp Arg Arg Gly  
290 295 300

Ile Leu Pro Leu Glu Glu Ser Gly Ser Arg Pro Pro Ser Thr Gln  
305 310 315

Glu Thr Ser Ser Ser Leu Leu Pro Gln Ser Pro Ala Pro Thr Glu  
320 325 330

His Leu Asn Ser Asn Glu Met Pro Glu Asp Ser Ser Thr Pro Glu  
335 340 345

Glu Met Pro Pro Pro Glu Pro Pro Glu Pro Pro Gln Glu Ala Ala  
350 355 360

Glu Ala Glu Lys

<210> 515

<211> 255

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 36, 38, 88, 118, 135, 193, 213, 222

<223> unknown base

<400> 515

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tgaattaggt attataggga tgggtggggtt gattttntt cctggaggct 100

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cccctgggtg gggaattgtg ttggaaagag gaactaccgc tanttctacc 200

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atcgt 255

<210> 516

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 516

caacgtgatt tcaaagctgg gctc 24

<210> 517

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 517

gcctcgatc aagaattcc 20

<210> 518

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 518

agtggaagtc gacctccc 18

<210> 519

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 519

ctcacctgaa atctctcata gccc 24

<210> 520

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 520

cgcaaaaccc atttgggag caggaattcc aatcatgtct gtgatggtgg 50

<210> 521

<211> 1679

<212> DNA

<213> Homo sapiens

<400> 521

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caaaaaagaa gaaaaagaag aagaaaaaaa atcatgaaa ccatccagcc 150  
aaaaatgcac aattctatct cttgggcaat cttcacgggg ctggctgctc 200  
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aaagctatgg acaacgtgac ggtccggcag ggggagagcg ccaccctcag 300  
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tgtgtatgac gagggccctt acacctgctc ggtgcagaca gacaaccacc 500  
caaagacctc tagggccac ctcattgtgc aagtatctcc caaaattgta 550  
gagatttctt cagatatctc cattaatgaa gggaacaata ttagcctcac 600  
ctgcatagca actggtagac cagagcctac ggttacttg agacacatct 650  
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cgtggccgcg cccgtggtac ggagagtaaa ggtcaccgtg aactatccac 800  
catacatttc agaagccaag ggtacaggtg tccccgtggg aaaaagggg 850  
aactgcagt gtgaagcctc agcagtcctc tcagcagaat tccagtggta 900  
caaggatgac aaaagactga ttgaaggaaa gaaaggggtg aaagtggaaa 950  
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gccgccacca ccaccacca cacaacagca atggcaacac cgacagcaac 1250



caatcagata tatacaaatg aaattagaag aaacacagcc tcatgggaca 1300

gaaatttgag ggaggggaac aaagaatact ttggggggaa aagagtttta 1350

aaaaagaaat tgaaaattgc cttgcagata ttaggtaca atggagtttt 1400

ctttcccaa acgggaagaa cacagcacac ccggcttgga cccactgcaa 1450

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<211> 344

<212> PRT

<213> Homo sapiens

<400> 522

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Thr Val Arg Gln Gly Glu Ser Ala Thr Leu Arg Cys Thr Ile Asp

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Asn Arg Val Thr Arg Val Ala Trp Leu Asn Arg Ser Thr Ile Leu

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Tyr Ala Gly Asn Asp Lys Trp Cys Leu Asp Pro Arg Val Val Leu

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Leu Ser Asn Thr Gln Thr Gln Tyr Ser Ile Glu Ile Gln Asn Val

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Asp Val Tyr Asp Glu Gly Pro Tyr Thr Cys Ser Val Gln Thr Asp  
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Asn His Pro Lys Thr Ser Arg Val His Leu Ile Val Gln Val Ser  
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Pro Lys Ile Val Glu Ile Ser Ser Asp Ile Ser Ile Asn Glu Gly  
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Asn Asn Ile Ser Leu Thr Cys Ile Ala Thr Gly Arg Pro Glu Pro  
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Thr Val Thr Trp Arg His Ile Ser Pro Lys Ala Val Gly Phe Val  
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Ser Glu Asp Glu Tyr Leu Glu Ile Gln Gly Ile Thr Arg Glu Gln  
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Ser Gly Asp Tyr Glu Cys Ser Ala Ser Asn Asp Val Ala Ala Pro  
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Val Val Arg Arg Val Lys Val Thr Val Asn Tyr Pro Pro Tyr Ile  
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Ser Glu Ala Lys Gly Thr Gly Val Pro Val Gly Gln Lys Gly Thr  
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Leu Gln Cys Glu Ala Ser Ala Val Pro Ser Ala Glu Phe Gln Trp  
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Tyr Lys Asp Asp Lys Arg Leu Ile Glu Gly Lys Lys Gly Val Lys  
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Val Glu Asn Arg Pro Phe Leu Ser Lys Leu Ile Phe Phe Asn Val  
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Ser Glu His Asp Tyr Gly Asn Tyr Thr Cys Val Ala Ser Asn Lys  
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Leu Gly His Thr Asn Ala Ser Ile Met Leu Phe Gly Pro Gly Ala  
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<211> 736

<212> PRT

<213> Homo sapiens

<400> 525

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Leu Gly Cys Leu Val Ala Leu Gly Val Gln Tyr His Arg Asp Pro  
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Ser His Ser Thr Cys Leu Thr Glu Ala Cys Ile Arg Val Ala Gly  
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Lys Ile Leu Glu Ser Leu Asp Arg Gly Val Ser Pro Cys Glu Asp  
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Phe Tyr Gln Phe Ser Cys Gly Gly Trp Ile Arg Arg Asn Pro Leu  
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Pro Asp Gly Arg Ser Arg Trp Asn Thr Phe Asn Ser Leu Trp Asp  
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Gln Asn Gln Ala Ile Leu Lys His Leu Leu Glu Asn Thr Thr Phe  
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Asn Ser Ser Ser Glu Ala Glu Gln Lys Thr Gln Arg Phe Tyr Leu  
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Ser Cys Leu Gln Val Glu Arg Ile Glu Glu Leu Gly Ala Gln Pro  
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Leu Arg Asp Leu Ile Glu Lys Ile Gly Gly Trp Asn Ile Thr Gly  
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Pro Trp Asp Gln Asp Asn Phe Met Glu Val Leu Lys Ala Val Ala  
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Gly Thr Tyr Arg Ala Thr Pro Phe Phe Thr Val Tyr Ile Ser Ala  
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Asp Ser Lys Ser Ser Asn Ser Asn Val Ile Gln Val Asp Gln Ser  
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Gly Leu Phe Leu Pro Ser Arg Asp Tyr Tyr Leu Asn Arg Thr Ala  
230 235 240

Asn Glu Lys Val Leu Thr Ala Tyr Leu Asp Tyr Met Glu Glu Leu  
245 250 255

Gly Met Leu Leu Gly Gly Arg Pro Thr Ser Thr Arg Glu Gln Met  
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Gln Gln Val Leu Glu Leu Glu Ile Gln Leu Ala Asn Ile Thr Val  
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Pro Gln Asp Gln Arg Arg Asp Glu Glu Lys Ile Tyr His Lys Met  
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Ser Ile Ser Glu Leu Gln Ala Leu Ala Pro Ser Met Asp Trp Leu  
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Ile Trp Asn Leu Val Gln Lys Thr Thr Ser Ser Leu Asp Arg Arg  
365 370 375

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575 580 585

Tyr Asp Lys Glu Gly Asn Leu Arg Pro Trp Trp Gln Asn Glu Ser  
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Leu Ala Ala Phe Arg Asn His Thr Ala Cys Met Glu Glu Gln Tyr  
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<211> 4308

<212> DNA

<213> Homo sapiens

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<223> unknown base

<400> 526

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<212> DNA

<213> Homo sapiens

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35 40 45

Met Met Val Arg Lys Gly Asp Thr Ala Val Leu Arg Cys Tyr Leu

50 55 60

Glu Asp Gly Ala Ser Lys Gly Ala Trp Leu Asn Arg Ser Ser Ile

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Ile Ser Thr Leu Asn Lys Arg Asp Tyr Ser Leu Gln Ile Gln Asn  
95                      100                      105

Val Asp Val Thr Asp Asp Gly Pro Tyr Thr Cys Ser Val Gln Thr  
110                      115                      120

Gln His Thr Pro Arg Thr Met Gln Val His Leu Thr Val Gln Val  
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Pro Pro Lys Ile Tyr Asp Ile Ser Asn Asp Met Thr Val Asn Glu  
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Gly Thr Asn Val Thr Leu Thr Cys Leu Ala Thr Gly Lys Pro Glu  
155                      160                      165

Pro Ser Ile Ser Trp Arg His Ile Ser Pro Ser Ala Lys Pro Phe  
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Glu Asn Gly Gln Tyr Leu Asp Ile Tyr Gly Ile Thr Arg Asp Gln  
185                      190                      195

Ala Gly Glu Tyr Glu Cys Ser Ala Glu Asn Ala Val Ser Phe Pro  
200                      205                      210

Asp Val Arg Lys Val Lys Val Val Val Asn Phe Ala Pro Thr Ile  
215                      220                      225

Gln Glu Ile Lys Ser Gly Thr Val Thr Pro Gly Arg Ser Gly Leu  
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Ile Arg Cys Glu Gly Ala Gly Val Pro Pro Pro Ala Phe Glu Trp  
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Tyr Lys Gly Glu Lys Lys Leu Phe Asn Gly Gln Gln Gly Ile Ile  
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Ile Gln Asn Phe Ser Thr Arg Ser Ile Leu Thr Val Thr Asn Val  
275                      280                      285

Thr Gln Glu His Phe Gly Asn Tyr Thr Cys Val Ala Ala Asn Lys

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Leu Gly Thr Thr Asn Ala Ser Leu Pro Leu Asn Pro Pro Ser Thr  
305 310 315

Ala Gln Tyr Gly Ile Thr Gly Ser Ala Asp Val Leu Phe Ser Cys  
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<210> 613

<211> 520

<212> PRT

<213> Homo Sapien

<400> 613

Met Arg Asn Lys Lys Ile Leu Lys Glu Asp Glu Leu Leu Ser Glu

1 5 10 15

Thr Gln Gln Ala Ala Phe His Gln Ile Ala Met Glu Pro Phe Glu

20 25 30

Ile Asn Val Pro Lys Pro Lys Arg Arg Asn Gly Val Asn Phe Ser

35 40 45

Leu Ala Val Val Val Ile Tyr Leu Ile Leu Leu Thr Ala Gly Ala

50 55 60

Gly Leu Leu Val Val Gln Val Leu Asn Leu Gln Ala Arg Leu Arg

65 70 75

Val Leu Glu Met Tyr Phe Leu Asn Asp Thr Leu Ala Ala Glu Asp

80 85 90

Ser Pro Ser Phe Ser Leu Leu Gln Ser Ala His Pro Gly Glu His

95 100 105

Leu Ala Gln Gly Ala Ser Arg Leu Gln Val Leu Gln Ala Gln Leu

110 115 120

Thr Trp Val Arg Val Ser His Glu His Leu Leu Gln Arg Val Asp

125 130 135

Asn Phe Thr Gln Asn Pro Gly Met Phe Arg Ile Lys Gly Glu Gln

140 145 150

Gly Ala Pro Gly Leu Gln Gly His Lys Gly Ala Met Gly Met Pro

155 160 165

Gly Ala Pro Gly Pro Pro Gly Pro Pro Ala Glu Lys Gly Ala Lys

170 175 180

Gly Ala Met Gly Arg Asp Gly Ala Thr Gly Pro Ser Gly Pro Gln

185 190 195

Gly Pro Pro Gly Val Lys Gly Glu Ala Gly Leu Gln Gly Pro Gln  
200 205 210

Gly Ala Pro Gly Lys Gln Gly Ala Thr Gly Thr Pro Gly Pro Gln  
215 220 225

Gly Glu Lys Gly Ser Lys Gly Asp Gly Gly Leu Ile Gly Pro Lys  
230 235 240

Gly Glu Thr Gly Thr Lys Gly Glu Lys Gly Asp Leu Gly Leu Pro  
245 250 255

Gly Ser Lys Gly Asp Arg Gly Met Lys Gly Asp Ala Gly Val Met  
260 265 270

Gly Pro Pro Gly Ala Gln Gly Ser Lys Gly Asp Phe Gly Arg Pro  
275 280 285

Gly Pro Pro Gly Leu Ala Gly Phe Pro Gly Ala Lys Gly Asp Gln  
290 295 300

Gly Gln Pro Gly Leu Gln Gly Val Pro Gly Pro Pro Gly Ala Val  
305 310 315

Gly His Pro Gly Ala Lys Gly Glu Pro Gly Ser Ala Gly Ser Pro  
320 325 330

Gly Arg Ala Gly Leu Pro Gly Ser Pro Gly Ser Pro Gly Ala Thr  
335 340 345

Gly Leu Lys Gly Ser Lys Gly Asp Thr Gly Leu Gln Gly Gln Gln  
350 355 360

Gly Arg Lys Gly Glu Ser Gly Val Pro Gly Pro Ala Gly Val Lys  
365 370 375

Gly Glu Gln Gly Ser Pro Gly Leu Ala Gly Pro Lys Gly Ala Pro  
380 385 390

Gly Gln Ala Gly Gln Lys Gly Asp Gln Gly Val Lys Gly Ser Ser  
395 400 405

Gly Glu Gln Gly Val Lys Gly Glu Lys Gly Glu Arg Gly Glu Asn  
410 415 420

Ser Val Ser Val Arg Ile Val Gly Ser Ser Asn Arg Gly Arg Ala  
425 430 435

Glu Val Tyr Tyr Ser Gly Thr Trp Gly Thr Ile Cys Asp Asp Glu  
440 445 450

Trp Gln Asn Ser Asp Ala Ile Val Phe Cys Arg Met Leu Gly Tyr  
455 460 465

Ser Lys Gly Arg Ala Leu Tyr Lys Val Gly Ala Gly Thr Gly Gln  
470 475 480

Ile Trp Leu Asp Asn Val Gln Cys Arg Gly Thr Glu Ser Thr Leu  
485 490 495

Trp Ser Cys Thr Lys Asn Ser Trp Gly His His Asp Cys Ser His  
500 505 510

Glu Glu Asp Ala Gly Val Glu Cys Ser Val  
515 520

<210> 614  
<211> 647  
<212> DNA  
<213> Homo Sapien

<400> 614  
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atttaagaag catcctctgc caagacaaa aggaaagaag aaaaagggcc 150  
aaaagccaaa atgaaactga tggctactgt ttccaccatt gggctaactt 200  
tgctgctagg agttcaagcc atgcctgcaa atgcctctc ttgctacaga 250  
aagatactaa aagatcaca ctgtcacaac ctccggaag gagtagctga 300  
cctgacacag attgatgtca atgtccagga tcatttctgg gatgggaagg 350  
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gttaaacaag tagtaataaa agttaattca atctaaaaaa aaaaaaa 647

<210> 615

<211> 98

<212> PRT

<213> Homo Sapien

<400> 615

Met Lys Leu Met Val Leu Val Phe Thr Ile Gly Leu Thr Leu Leu

1 5 10 15

Leu Gly Val Gln Ala Met Pro Ala Asn Arg Leu Ser Cys Tyr Arg

20 25 30

Lys Ile Leu Lys Asp His Asn Cys His Asn Leu Pro Glu Gly Val

35 40 45

Ala Asp Leu Thr Gln Ile Asp Val Asn Val Gln Asp His Phe Trp

50 55 60

Asp Gly Lys Gly Cys Glu Met Ile Cys Tyr Cys Asn Phe Ser Glu

65 70 75

Leu Leu Cys Cys Pro Lys Asp Val Phe Phe Gly Pro Lys Ile Ser

80 85 90

Phe Val Ile Pro Cys Asn Asn Gln

95

<210> 616

<211> 2558

<212> DNA

<213> Homo Sapien

<400> 616

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cagcctgcag ggctgataag cgaggcatta gtgagattga gagagacttt 100

accccgccgt ggtggttga gggcgcgag tagagcagca gcacaggcgc 150

gggtcccgaggccggctc tgctcgccc gagatgtga atctcttca 200

cgaaccgac tcggctgtgg ccaccgccc ccgcccgcg tggctgtgcg 250

ctggggcgct ggtgctggcg ggtggcttct ttctctcgg ctctcttctc 300

gggtggttta taaatctc caatgaagct actaacatta ctcaaagca 350

taatatgaaa gcatttttg atgaattgaa agctgagaac atcaagaagt 400

tcttacataa ttttacacag ataccacatt tagcaggaa agaacaaaac 450

ttcagcttg caaagcaat tcaatcccag tggaagaat ttggcctgga 500

ttctgttgag ctagctcatt atgatgtct gttgtctac ccaaataaga 550

ctcatcccaa ctacatctca ataattaatg aagatggaaa tgagatttctc 600

aacacatcat tattgaacc acctctcca ggatatgaaa atgttctgga 650

tattgtacca ctttcagtgc cttctctcc tcaaggaatg ccagaggcg 700

atctagtgtg tgtaactat gcacgaactg aagacttct taaattgaa 750

cgggacatga aaatcaattg ctctgggaaa attgtaattg ccagatatgg 800

gaaagtcttc agaggaaata aggttaaaaa tgcccagctg gcaggggcca 850

aaggagtcat tctctactcc gacctgtgc actactttgc tctgggggtg 900

aagtcctatc cagacggttg gaatcttct ggaggtggtg tccagcgtgg 950

aaatatccta aatctgaatg gtgcaggaga ccctctcaca ccaggttacc 1000

cagcaaatga atatgcttat aggcgtggaa ttgcagaggc tgttggtctt 1050

ccaagtattc ctgttcatcc aattggatac tatgatgcac agaagctct 1100

agaaaaaatg ggtggctcag caccaccaga tagcagctgg agaggaagtc 1150

tcaaagtgcc ctacaatgtt ggacctggct ttactggaaa ctttctaca 1200

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atatataa 2558

<210> 617

<211> 750

<212> PRT

<213> Homo Sapien

<400> 617

Met Trp Asn Leu Leu His Glu Thr Asp Ser Ala Val Ala Thr Ala  
1 5 10 15

Arg Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu Val Leu Ala Gly  
20 25 30

Gly Phe Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser  
35 40 45

Ser Asn Glu Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala  
50 55 60

Phe Leu Asp Glu Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu His  
65 70 75

Asn Phe Thr Gln Ile Pro His Leu Ala Gly Thr Glu Gln Asn Phe  
80 85 90

Gln Leu Ala Lys Gln Ile Gln Ser Gln Trp Lys Glu Phe Gly Leu  
95 100 105

Asp Ser Val Glu Leu Ala His Tyr Asp Val Leu Leu Ser Tyr Pro  
110 115 120

Asn Lys Thr His Pro Asn Tyr Ile Ser Ile Ile Asn Glu Asp Gly  
125 130 135

Asn Glu Ile Phe Asn Thr Ser Leu Phe Glu Pro Pro Pro Gly  
140 145 150

Tyr Glu Asn Val Ser Asp Ile Val Pro Pro Phe Ser Ala Phe Ser



155	160	165
Pro Gln Gly Met Pro Glu Gly Asp Leu Val Tyr Val Asn Tyr Ala		
170	175	180
Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg Asp Met Lys Ile Asn		
185	190	195
Cys Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly Lys Val Phe Arg		
200	205	210
Gly Asn Lys Val Lys Asn Ala Gln Leu Ala Gly Ala Lys Gly Val		
215	220	225
Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Gly Val Lys		
230	235	240
Ser Tyr Pro Asp Gly Trp Asn Leu Pro Gly Gly Gly Val Gln Arg		
245	250	255
Gly Asn Ile Leu Asn Leu Asn Gly Ala Gly Asp Pro Leu Thr Pro		
260	265	270
Gly Tyr Pro Ala Asn Glu Tyr Ala Tyr Arg Arg Gly Ile Ala Glu		
275	280	285
Ala Val Gly Leu Pro Ser Ile Pro Val His Pro Ile Gly Tyr Tyr		
290	295	300
Asp Ala Gln Lys Leu Leu Glu Lys Met Gly Gly Ser Ala Pro Pro		
305	310	315
Asp Ser Ser Trp Arg Gly Ser Leu Lys Val Pro Tyr Asn Val Gly		
320	325	330
Pro Gly Phe Thr Gly Asn Phe Ser Thr Gln Lys Val Lys Met His		
335	340	345
Ile His Ser Thr Asn Glu Val Thr Arg Ile Tyr Asn Val Ile Gly		
350	355	360
Thr Leu Arg Gly Ala Val Glu Pro Asp Arg Tyr Val Ile Leu Gly		
365	370	375
Gly His Arg Asp Ser Trp Val Phe Gly Gly Ile Asp Pro Gln Ser		

380

385

390

Gly Ala Ala Val Val His Glu Ile Val Arg Ser Phe Gly Thr Leu

395

400

405

Lys Lys Glu Gly Trp Arg Pro Arg Arg Thr Ile Leu Phe Ala Ser

410

415

420

Trp Asp Ala Glu Glu Phe Gly Leu Leu Gly Ser Thr Glu Trp Ala

425

430

435

Glu Glu Asn Ser Arg Leu Leu Gln Glu Arg Gly Val Ala Tyr Ile

440

445

450

Asn Ala Asp Ser Ser Ile Glu Gly Asn Tyr Thr Leu Arg Val Asp

455

460

465

Cys Thr Pro Leu Met Tyr Ser Leu Val His Asn Leu Thr Lys Glu

470

475

480

Leu Lys Ser Pro Asp Glu Gly Phe Glu Gly Lys Ser Leu Tyr Glu

485

490

495

Ser Trp Thr Lys Lys Ser Pro Ser Pro Glu Phe Ser Gly Met Pro

500

505

510

Arg Ile Ser Lys Leu Gly Ser Gly Asn Asp Phe Glu Val Phe Phe

515

520

525

Gln Arg Leu Gly Ile Ala Ser Gly Arg Ala Arg Tyr Thr Lys Asn

530

535

540

Trp Glu Thr Asn Lys Phe Ser Gly Tyr Pro Leu Tyr His Ser Val

545

550

555

Tyr Glu Thr Tyr Glu Leu Val Glu Lys Phe Tyr Asp Pro Met Phe

560

565

570

Lys Tyr His Leu Thr Val Ala Gln Val Arg Gly Gly Met Val Phe

575

580

585

Glu Leu Ala Asn Ser Ile Val Leu Pro Phe Asp Cys Arg Asp Tyr

590

595

600

Ala Val Val Leu Arg Lys Tyr Ala Asp Lys Ile Tyr Ser Ile Ser

605	610	615
Met Lys His Pro Gln Glu Met Lys Thr Tyr Ser Val Ser Phe Asp		
620	625	630
Ser Leu Phe Ser Ala Val Lys Asn Phe Thr Glu Ile Ala Ser Lys		
635	640	645
Phe Ser Glu Arg Leu Gln Asp Phe Asp Lys Ser Asn Pro Ile Val		
650	655	660
Leu Arg Met Met Asn Asp Gln Leu Met Phe Leu Glu Arg Ala Phe		
665	670	675
Ile Asp Pro Leu Gly Leu Pro Asp Arg Pro Phe Tyr Arg His Val		
680	685	690
Ile Tyr Ala Pro Ser Ser His Asn Lys Tyr Ala Gly Glu Ser Phe		
695	700	705
Pro Gly Ile Tyr Asp Ala Leu Phe Asp Ile Glu Ser Lys Val Asp		
710	715	720
Pro Ser Lys Ala Trp Gly Glu Val Lys Arg Gln Ile Tyr Val Ala		
725	730	735
Ala Phe Thr Val Gln Ala Ala Ala Glu Thr Leu Ser Glu Val Ala		
740	745	750

<210> 618

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 618

agatgtgaag gtgcaggtgt gccg 24

<210> 619

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 619

gaacatcagc gctcccgta attcc 25

<210> 620

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 620

ccagcctttg aatggtacaa aggagagaag aagctcttca atggcc 46

<210> 621

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 621

ccaaactcac ccagtgagtg tgagc 25

<210> 622

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 622

tgggaaatca ggaatggtgt tctcc 25

<210> 623

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide probe

<400> 623

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